

Fig. 1

| | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5' | 9 | | | 18 | | | 27 | | | 36 | | | 45 | | | 54 | | |
| | GTG | GGC | ATG | GTG | GGC | AAC | GTC | CTG | CTG | GTG | CTG | GTG | ATC | GCG | CGG | GTG | CGC | CGG |
| | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | Val | Gly | Met | Val | Gly | Asn | Val | Leu | Leu | Val | Leu | Val | Ile | Ala | Arg | Val | Arg | Arg |
| | 63 | | | 72 | | | 81 | | | 90 | | | 99 | | | 108 | | |
| | CTG | CAC | AAC | GTG | ACG | AAC | TTC | CTC | ATC | GGC | AAC | CTG | GCC | TTG | TCC | GAC | GTG | CTC |
| | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | Leu | His | Asn | Val | Thr | Asn | Phe | Leu | Ile | Gly | Asn | Leu | Ala | Leu | Ser | Asp | Val | Leu |
| | 117 | | | 126 | | | 135 | | | 144 | | | 153 | | | 162 | | |
| | ATG | TGC | ACC | GCC | TGC | GTG | CCG | CTC | ACG | CTG | GCC | TAT | GCC | TTC | GAG | CCA | CGC | GGC |
| | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | Met | Cys | Thr | Ala | Cys | Val | Pro | Leu | Thr | Leu | Ala | Tyr | Ala | Phe | Glu | Pro | Arg | Gly |
| | 171 | | | 180 | | | 189 | | | 198 | | | 207 | | | 216 | | |
| | TGG | GTG | TTC | GGC | GGC | GGC | CTG | TGC | CAC | CTG | GTC | TTC | TTC | CTG | CAG | CCG | GTC | ACC |
| | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | Trp | Val | Phe | Gly | Gly | Gly | Leu | Cys | His | Leu | Val | Phe | Phe | Leu | Gln | Pro | Val | Thr |
| | 225 | | | 234 | | | 243 | | | 252 | | | 261 | | | 270 | | |
| | GTC | TAT | GTG | TCG | GTG | TTC | ACG | CTC | ACC | ACC | ATC | GCA | GTG | GAC | CGG | TAC | GTC | GTG |
| | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | Val | Tyr | Val | Ser | Val | Phe | Thr | Leu | Thr | Thr | Ile | Ala | Val | Asp | Arg | Tyr | Val | Val |
| | 279 | | | 288 | | | 297 | | | | | | | | | | | |
| | CTG | GTG | CAC | CCG | CTG | AGG | CGG | CGC | ATC | 3' | | | | | | | | |
| | --- | --- | --- | --- | --- | --- | --- | --- | --- | | | | | | | | | |
| | Leu | Val | His | Pro | Leu | Arg | Arg | Arg | Ile | | | | | | | | | |

Fig. 2

5' 9 18 27 36 45 54
 GGC CTG CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr

 63 72 81 90 99 108
 GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG GTG CCG GGC TGC GTG ACC CAG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln

 117 126 135 144 153 162
 AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val

 171 180 189 198
 GTG GTC GTG GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr

002250 0529/550

Fig. 3

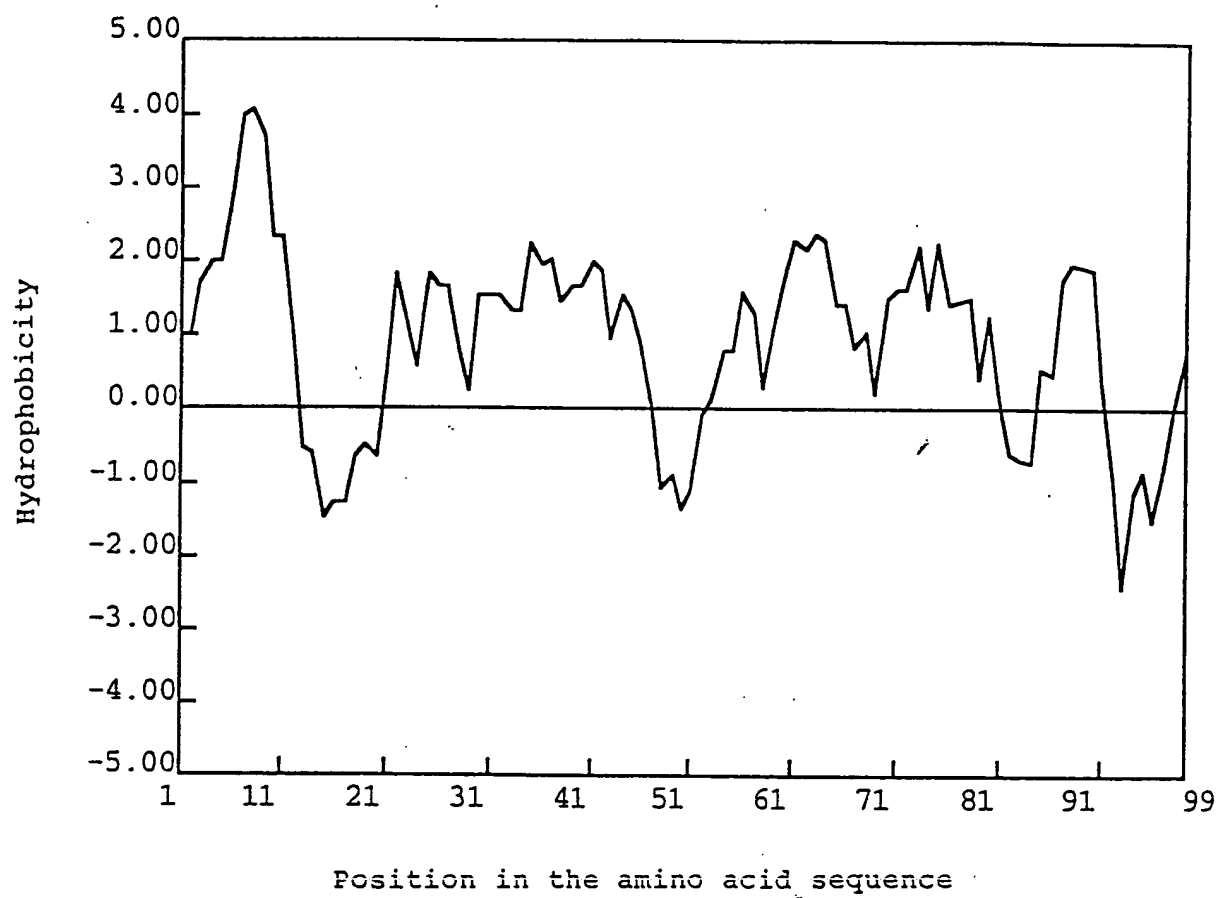


Fig. 4

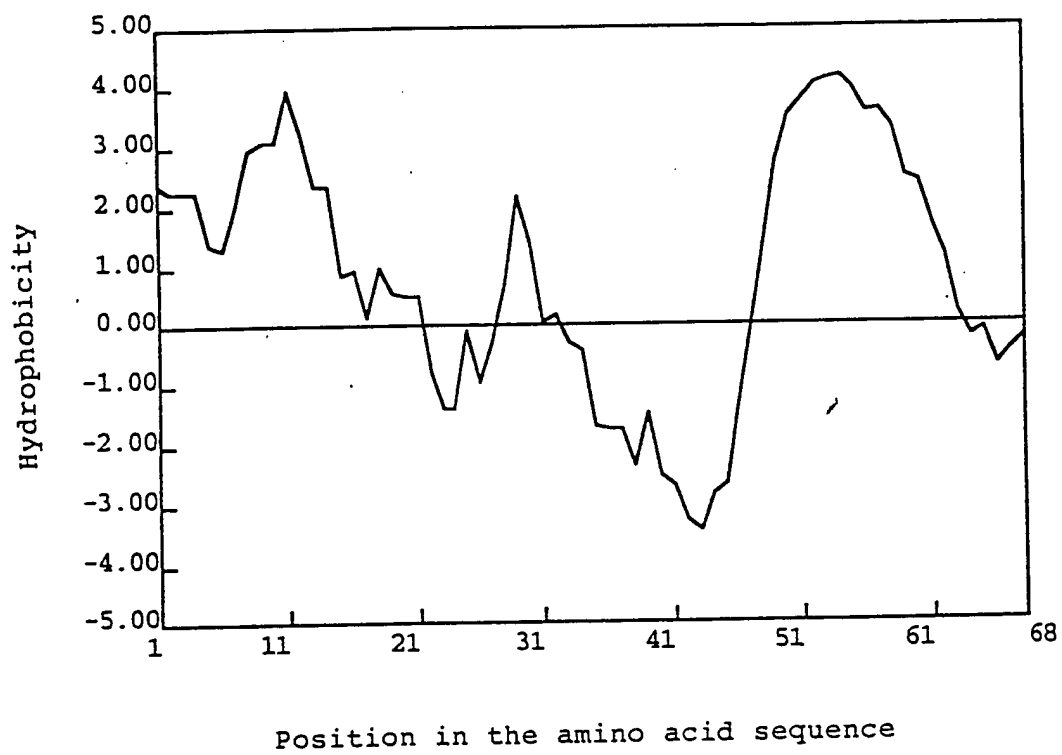


Fig. 5

| | | | | | | | | | | | |
|--------|-----|-----|-----|----|-----|----|-----|----|-----|----|-----|
| P19P2 | 1 | VGV | 10 | LV | 20 | LV | 30 | AL | 40 | CV | 50 |
| S12863 | 1 | LV | 10 | LV | 20 | LV | 30 | AL | 40 | CV | 50 |
| P19P2 | 1 | VGV | 10 | LV | 20 | LV | 30 | AL | 40 | CV | 50 |
| S12863 | 1 | LV | 10 | LV | 20 | LV | 30 | AL | 40 | CV | 50 |
| P19P2 | 51 | MDH | 60 | LV | 70 | LV | 80 | LV | 90 | LV | 100 |
| S12863 | 51 | MDH | 60 | LV | 70 | LV | 80 | LV | 90 | LV | 100 |
| P19P2 | 101 | NRH | 110 | LV | 120 | LV | 130 | LV | 140 | LV | 150 |
| S12863 | 101 | NRH | 110 | LV | 120 | LV | 130 | LV | 140 | LV | 150 |
| P19P2 | 151 | FP | 160 | LV | 170 | LV | 180 | LV | 190 | LV | 200 |
| S12863 | 151 | FP | 160 | LV | 170 | LV | 180 | LV | 190 | LV | 200 |
| P19P2 | 201 | AD | 210 | LV | 220 | LV | 230 | LV | 240 | LV | 250 |
| S12863 | 201 | AD | 210 | LV | 220 | LV | 230 | LV | 240 | LV | 250 |

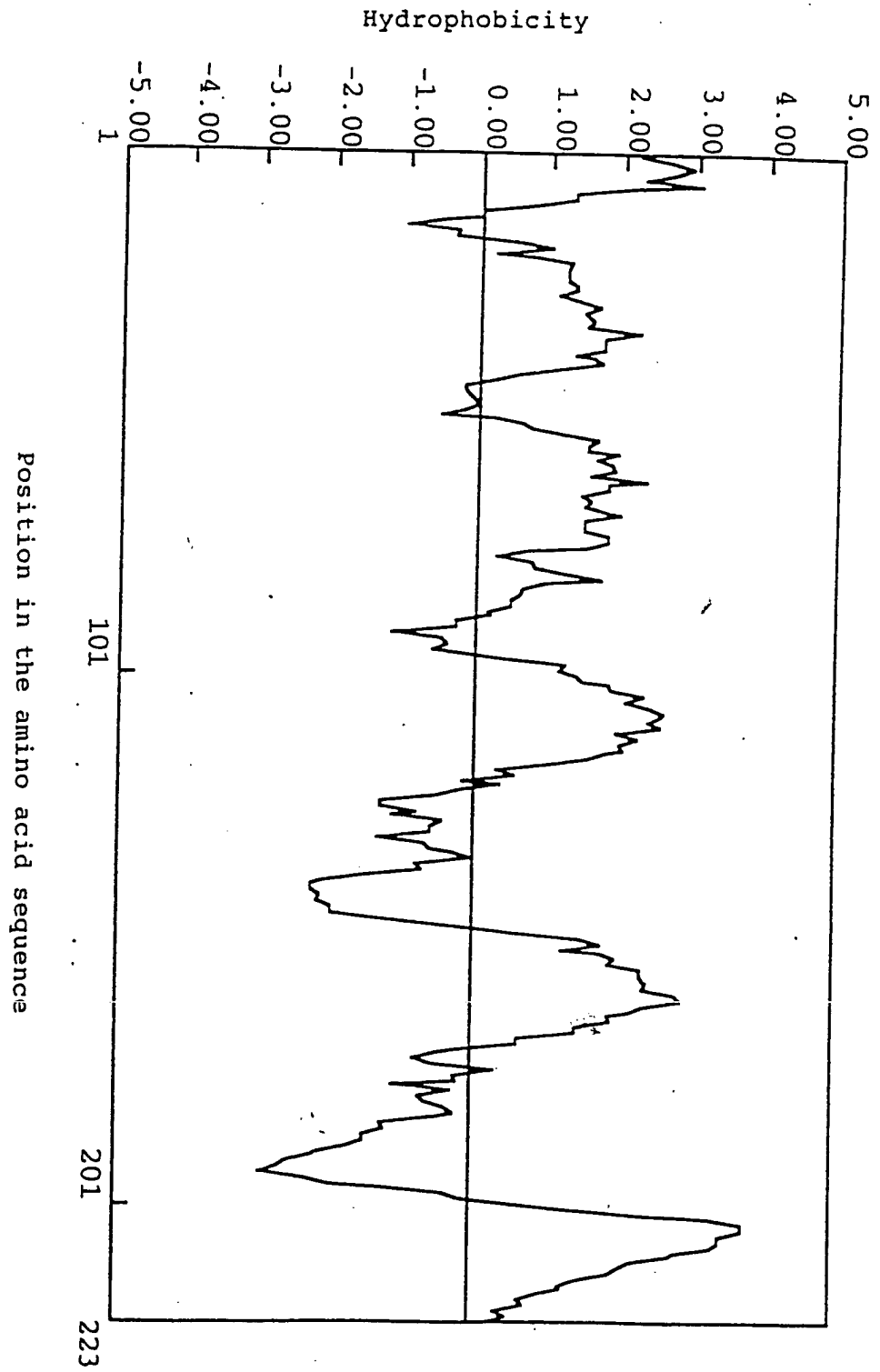
| | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|---|
| | | 657 | | | 666 | | |
| CTC | TGC | TGG | CTC | CCC | TTC | TTC | 3 |
| --- | --- | --- | --- | --- | --- | --- | |
| Leu | Cys | Trp | Leu | Pro | Phe | Phe | |

2025

Fig. 7

| | | | | | | | | | | | |
|--------------|-----|-------------|-----|-------------|-----|-------------|-----|-------------|-----|--------------|-----|
| p19P2 | 1 | VGWVGNNLLV | 10 | LVTVARVRRLH | 20 | NVTNELLIGNL | 30 | ALSDVLEMTTA | 40 | CVEPLTLAYAF | 50 |
| pg3-2/pg1-10 | 1 | VGWVGNNLLV | 10 | LVTVARVRRLH | 20 | NVTNELLIGNL | 30 | ALSDVLEMTTA | 40 | CVEPLTLAYAF | 50 |
| p19P2 | 51 | EPRCMVFEggG | 60 | LCHLVFEFLQ | 70 | VTVYVSVEFTL | 80 | TTIAVDRLRYV | 90 | LVHPLRLRI | 100 |
| pg3-2/pg1-10 | 51 | EPRCMVFEggG | 60 | LCHLVFEFLQ | 70 | VTVYVSVEFTL | 80 | TTIAVDRLRYV | 90 | LVHPLRLRI | 100 |
| p19P2 | 101 | ----- | 110 | ----- | 120 | ----- | 130 | ----- | 140 | ----- | 150 |
| pg3-2/pg1-10 | 101 | LRLSAYAVLA | 110 | IWVLSAVIAL | 120 | PAVHTYHVE | 130 | LKPHDRLCE | 140 | EFWGSQERQR | 150 |
| p19P2 | 151 | ----- | 160 | TYLLPPLLVIL | 170 | LSYVRVSVKTL | 180 | RNRVVFPGCVT | 190 | QSQAADWDPRAR | 200 |
| pg3-2/pg1-10 | 151 | QLYAWGILLV | 160 | TYLLPPLLVIL | 170 | LSYVRVSVKTL | 180 | RNRVVFPGCVT | 190 | QSQAADWDPRAR | 200 |
| p19P2 | 201 | RRRTFCLLVV | 210 | VWVFEATCWL | 220 | PYY..... | 230 | | 240 | | 250 |
| pg3-2/pg1-10 | 201 | RRRTFCLLVV | 210 | VWVFEATCWL | 220 | PYY..... | 230 | | 240 | | 250 |

Fig. 8



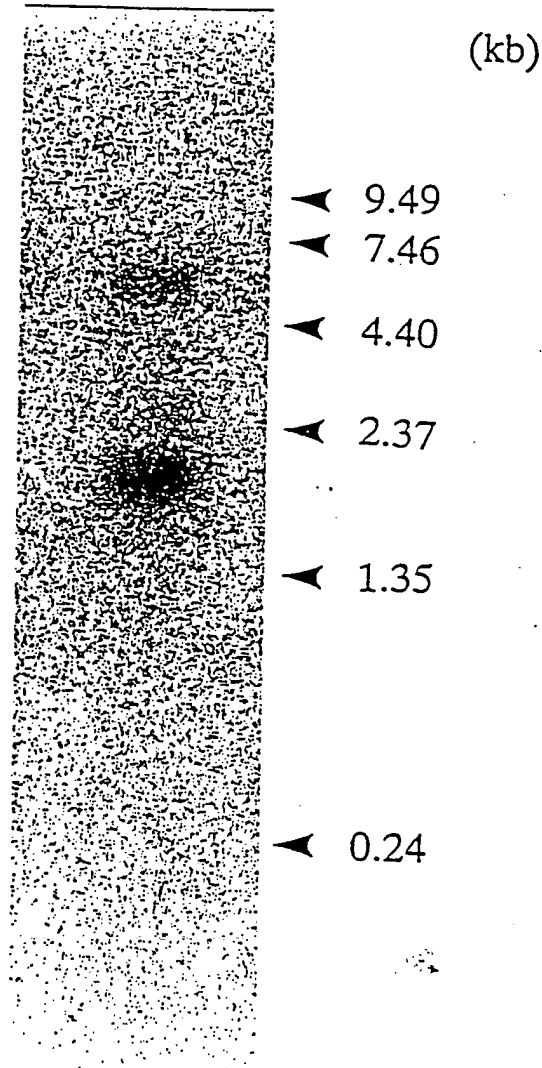
09576290.052300

Fig. 9

| | | |
|------|---|-------|
| 1 | CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT | 60 |
| 1 | | 1 |
| 61 | CTGCCCCCTTCTCCCGCGAGTGCTTCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG | 120 |
| 1 | | Met 1 |
| 121 | GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCGCCGGCG | 180 |
| 1 | AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla | 21 |
| 181 | GTCACAACCTCCCGCCAACAGAGCGCAGAGGCTCGGCGGGCAACGGGTGGTGGCTGGC | 240 |
| 21 | ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly | 41 |
| 241 | GCGGACGCTCCAGCCGTACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG | 300 |
| 41 | AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly | 61 |
| 301 | CTGATCGTGTCTCTACAGCGTCTGGTGGTCTGGTGGGCTGGTGGGCAACTGCCTGCTG | 360 |
| 61 | LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu | 81 |
| 361 | GTGCTGGTGATCGCGCGGGTGGCGGGCTGCACAACGTGACGAACCTTCTCATCGGCAAC | 420 |
| 81 | ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn | 101 |
| 421 | CTGGCCTGTGCCAGCTGTCTATGTGCACCGCTGCGTGGCGCTCAGCGTGGCCTATGCC | 480 |
| 101 | LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla | 121 |
| 481 | TTCGAGCCACGCGGCTGGGTGTTCGGCGGGCGGCTGTGCCACCTGGTCTTCTTCTGCAG | 540 |
| 121 | PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln | 141 |
| 541 | CCGGTCACCGTCTATGTGTGGTGTTCACGCTCACCACCATCGCAGTGGACCGCTACGTC | 600 |
| 141 | ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal | 161 |
| 501 | GTGCTGGTGACCCGCTGAGGCGGCGCATCTCGCTGGCGCTCAGCGCTACGCTGTGCTG | 660 |
| 161 | ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu | 181 |
| 561 | GCCATCTGGCGCTGTCCGCGGTGTGGCGGTGCCCGCGCGCTGCACACCTATCAGTG | 720 |
| 181 | AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal | 201 |
| 721 | GAGCTCAAGCCGACGACGTGCGCTCTGCGAGGAGTTCTGGGGCTCCAGGAGCGCCAG | 780 |
| 201 | GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln | 221 |
| 781 | CGCCAGCTCTACGCTGGGGCTGTGCTGGTACCTACCTGCTCCCTCTGCTGGTCATC | 840 |
| 221 | ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle | 241 |
| 841 | CTCCTGTCTTACGTCCGGGTGTGAGTGAAGCTCCGCAACCGCGTGGTGGCGGGCTGCGTG | 900 |
| 241 | LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal | 261 |
| 901 | ACCCAGAGCCAGGCGGACTGGGACCGCGCTCGGCGCGGCGCACCTTCTGCTTGCTGGTG | 960 |
| 261 | ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal | 281 |
| 961 | GTGGTCGTGGTGGTGTTCGCCGTCTGCTGGCTGCCGCTGCACGCTTCAACCTGCTGCGG | 1020 |
| 281 | ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg | 301 |
| 1021 | GACCTCGACCCCAAGCCATCGACCCTTACGCCCTTGGGCTGGTGAGCTGCTCTGCCAC | 1080 |
| 301 | AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis | 321 |
| 1081 | TGGCTCGCCATGAGTTCCGCCCTGTACAACCCCTTCACTACGCTGGCTGCACGACAGC | 1140 |
| 321 | TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer | 341 |
| 1141 | TTCCGCGAGGAGCTGCGCAAACTGTTGGTCTGCTGGCCCCGCAAGATAGCCCCCATGGC | 1200 |
| 341 | PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly | 361 |
| 1201 | CAGAATATGACCGTCAGCGTGGTCACTCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC | 1260 |
| 361 | GlnAsnMetThrValSerValValIle*** | 371 |
| 1261 | TCCACTTCAACTGGCCTCTAGGGCACCCTCGAGGTCAATCTGGTGCTTATTCTCAGCA | 1320 |
| 371 | | 371 |
| 1321 | CCAGAGCTAGC | 1331 |
| 371 | | 371 |

00576250 052300

Fig. 10



005250-0629/550

Fig. 11

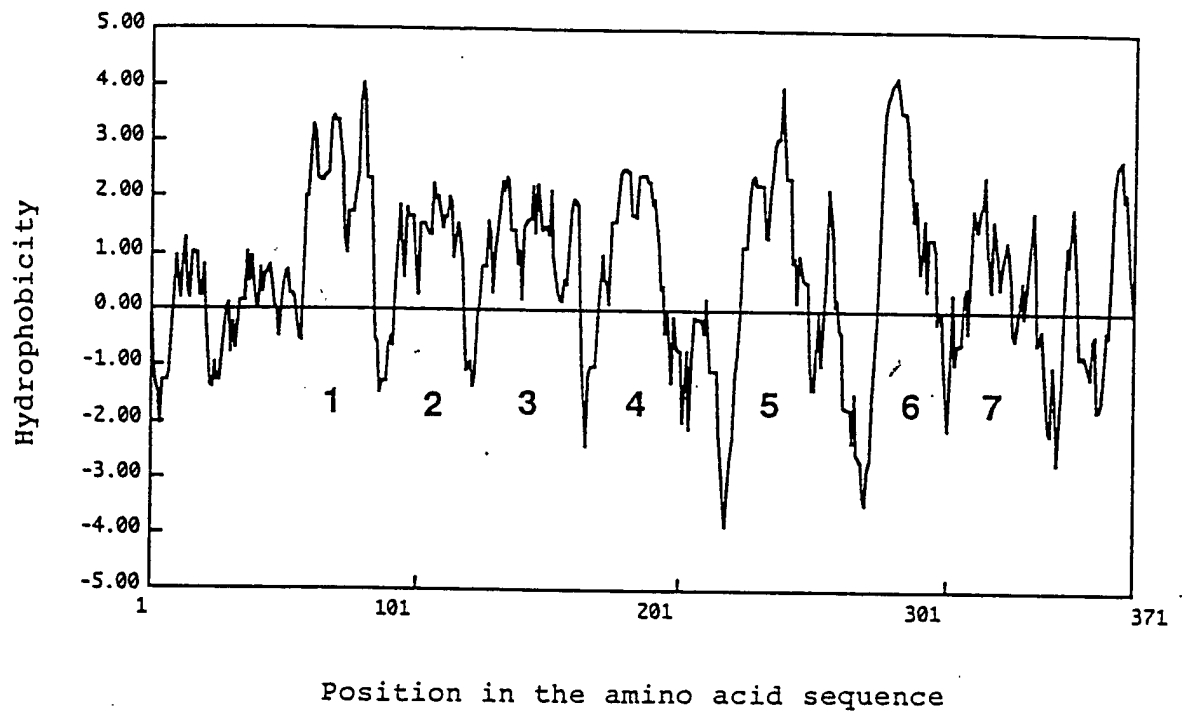


Fig. 12

| | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 5' | CTG | TGT | 9 | ATC | GCG | 18 | GTG | GAT | 27 | AGG | TAC | GTG | GTT | 36 | CTG | GTG | CAC | 45 | CCG | CTA | CGT | 54 | CGG |
| | Leu | Cys | Val | Ile | Ala | Val | Asp | Arg | Tyr | Val | Val | Leu | Val | His | Pro | Leu | Arg | Arg | | | | | |
| | CGC | ATT | 63 | TCA | CTG | AGG | CTC | AGC | 81 | GCC | TAC | GCG | GTG | 90 | CTG | GGC | ATC | 99 | TGG | GCT | CTA | 108 | TCT |
| | Arg | Ile | Ser | Leu | Arg | Leu | Ser | Ala | Tyr | Ala | Val | Leu | Gly | Ile | Trp | Ala | Leu | Ser | | | | | |
| | GCA | GTG | 117 | CTG | GCG | CTG | CCG | GCC | 126 | GCG | GTG | 135 | CAC | ACC | 144 | TAC | CAT | 153 | GTG | GAG | CTC | 162 | CCC |
| | Ala | Val | Leu | Ala | Leu | Pro | Ala | Ala | Val | His | Thr | Tyr | His | Val | Glu | Leu | Lys | Pro | | | | | |
| | CAC | GAC | 171 | GTG | AGC | CTC | TGC | GAG | 180 | GAG | GAG | 189 | TTC | TGG | GGC | TCG | CAG | GAG | 207 | CGC | CAA | CGC | 216 |
| | His | Asp | Val | Ser | Leu | Cys | Glu | Glu | Phe | Trp | Gly | Ser | Gln | Glu | Arg | Gln | Arg | Gln | | | | | |
| | ATC | TAC | 225 | GCC | TGG | GGG | CTG | CTT | 234 | CTG | GGC | ACC | TAT | 243 | TTG | CTC | CCC | 252 | CTG | CTG | GCC | 261 | ATC |
| | Ile | Tyr | Ala | Trp | Gly | Leu | Leu | Leu | Gly | Thr | Tyr | Leu | Leu | Pro | Leu | Leu | Ala | Ile | | | | | |
| | CTC | CTG | 279 | TCT | TAC | GTA | CGG | GTG | 288 | TCA | GTG | AAG | CTG | 306 | AGG | AAC | CGC | 315 | GTG | GTG | CCT | 324 | GGC |
| | Leu | Leu | Ser | Tyr | Val | Arg | Val | Ser | Val | Lys | Leu | Arg | Asn | Arg | Val | Val | Pro | Gly | | | | | |
| | AGC | GTG | 333 | ACC | CAG | AGT | CAA | GCT | 342 | GAC | TGG | GAC | CGA | 351 | GCG | CGT | CGC | 360 | CGC | CGC | ACT | 369 | TTC |
| | Ser | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala | Arg | Arg | Arg | Arg | Thr | Phe | | | | | |
| | TGT | CTG | 387 | GTG | GTG | GTG | GTG | GTA | 396 | GTG | TTC | ACG | CTC | 405 | TGC | TGG | CTG | 414 | CCC | TTC | 423 | 432 | TAC |
| | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | Phe | Thr | Leu | Cys | Trp | Leu | Pro | Phe | Tyr | | | | | |

CT 3'

Fig. 13

p19P2
pg3-2/pg1-10
p5S38

| | | | | | | | | | | |
|-----|------------|----|-------------|----|------------|----|------------|----|------------|-----|
| 1 | VGMVGNVLIV | 10 | LVITARVRRLH | 20 | NVTNFIIGNL | 30 | ALSDVIMCTA | 40 | CVPLTLAYAF | 50 |
| 1 | VGMVGNILIV | | LVITARVRRLY | | NVTNFIIGNL | | ALSDVIMCTA | | CVPLTLAYAF | |
| -79 | | | | | | | | | | -30 |

p19P2
pg3-2/pg1-10
p5S38

| | | | | | | | | | | |
|-----|------------|----|------------|----|-------------|----|------------|----|-----------|-----|
| 51 | EPHGMVEGGG | 60 | LCHLVEFFLP | 70 | VTVYVSVEFTL | 80 | TTTAVDRIYV | 90 | LVHPLRRRI | 100 |
| 51 | EPHGMVEGGG | | LCHLVEFFLP | | VTVYVSVEFTL | | TTTAVDRIYV | | LVHPLRRRI | |
| -29 | | | | | | | CVLAVDRIYV | | LVHPLRRRI | 21 |

p19P2
pg3-2/pg1-10
p5S38

| | | | | | | | | | | |
|-----|------------|-----|------------|-----|------------|-----|------------|-----|------------|-----|
| 101 | LRLSAYAVLA | 110 | IMVLSAVLAL | 120 | PAVHTTYHVE | 130 | LKPHDYRLCE | 140 | EFWGSQEROR | 150 |
| 101 | LRLSAYAVLA | | IMVLSAVLAL | | PAVHTTYHVE | | LKPHDYRLCE | | EFWGSQEROR | |
| 22 | LRLSAYAVLS | | IMVLSAVLAL | | PAVHTTYHVE | | LKPHDYSLCE | | EFWGSQEROR | 71 |

p19P2
pg3-2/pg1-10
p5S38

| | | | | | | | | | | |
|-----|------------|-----|-------------|-----|-------------|-----|------------|-----|------------|-----|
| 151 | GLLIV | 160 | TYLLPLLVITL | 170 | LSYVRVSVKTL | 180 | RNRVVPGLVT | 190 | QSQADWDRAR | 200 |
| 151 | GLLIV | | TYLLPLLVITL | | LSYVRVSVKTL | | RNRVVPGLVT | | QSQADWDRAR | |
| 72 | QTYAMGLLIS | | TYLLPLLVITL | | LSYVRVSVKTL | | RNRVVPGLVT | | QSQADWDRAR | 121 |

p19P2
pg3-2/pg1-10
p5S38

| | | | | | | | | | | |
|-----|------------|-----|------------|-----|-----|-----|-------|-----|-------|-----|
| 201 | RRRTFCLLVV | 210 | VVVVFALCWL | 220 | PYY | 230 | | 240 | | 250 |
| 201 | RRRTFCLLVV | | VVVVFALCWL | | PYY | | | | | |
| 122 | RRRTFCLLVV | | VVVVFALCWL | | PYY | | | | | 171 |

Fig. 14

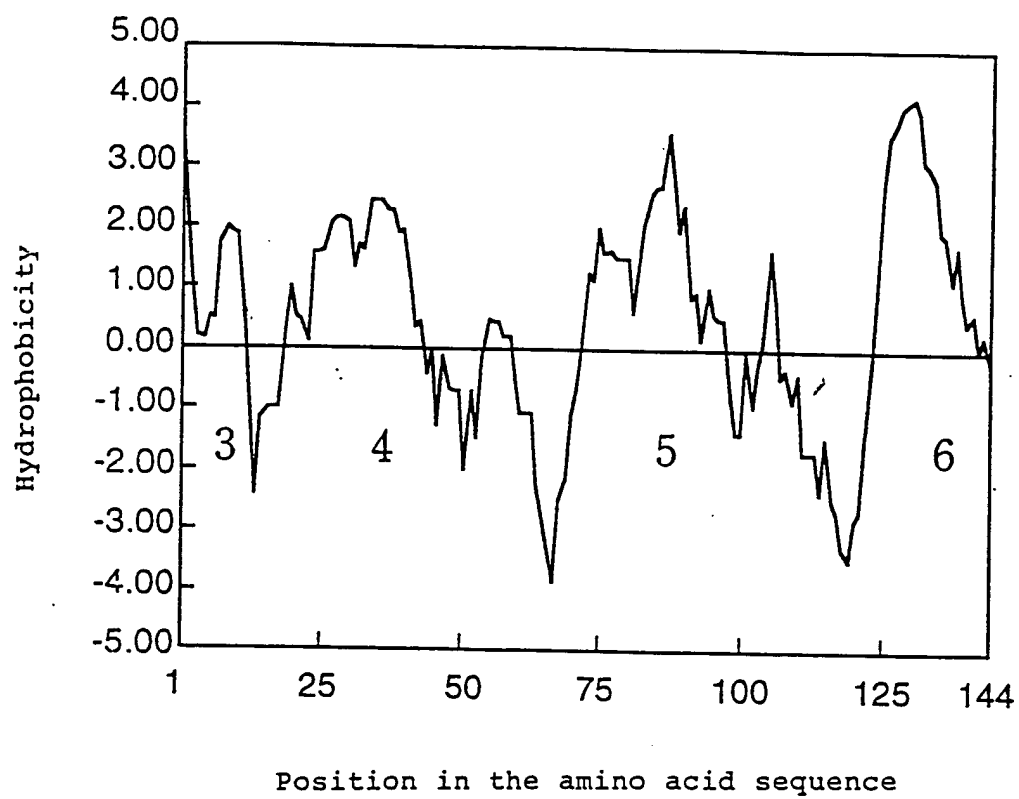
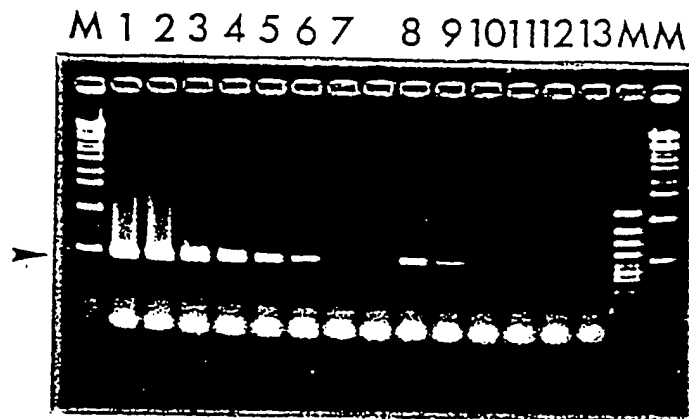
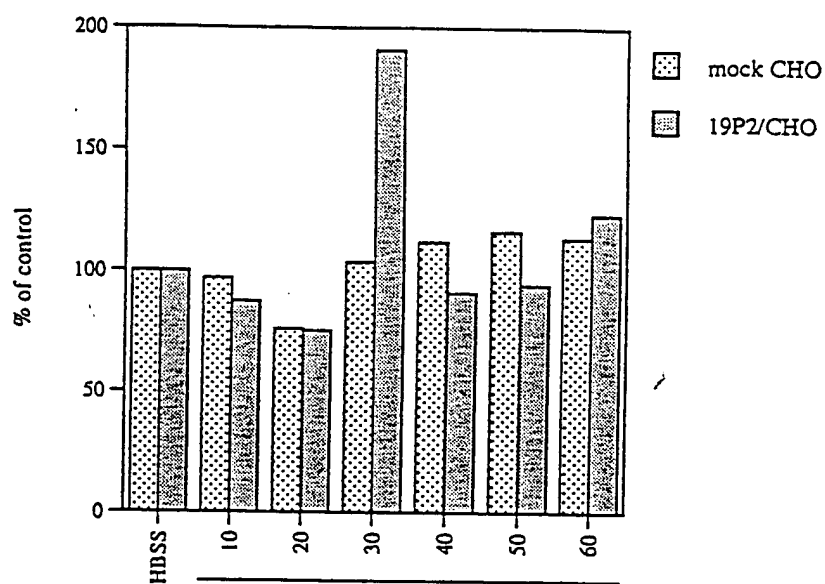


Fig. 15



006250 0523/550

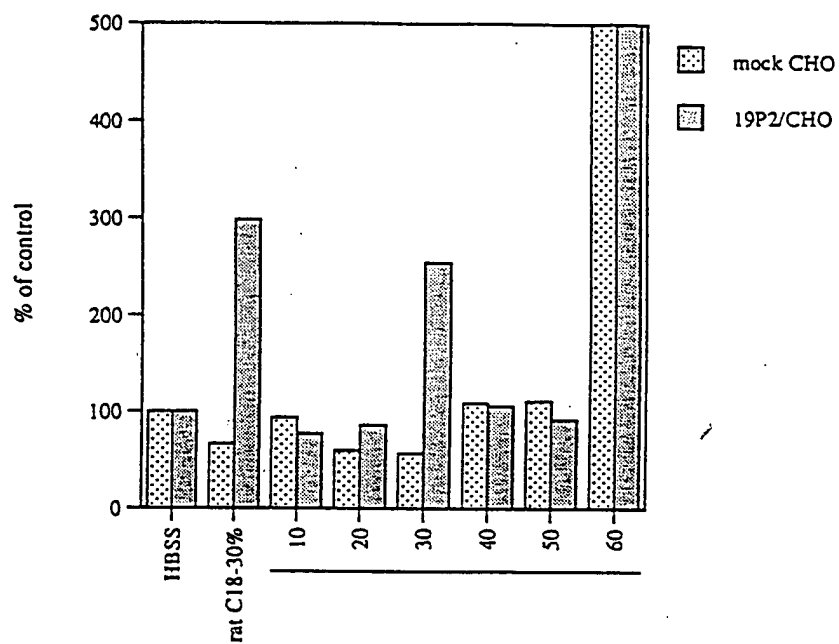
Fig. 16



rat whole brain extract

C₁₈-column CH₃CN elution (%)

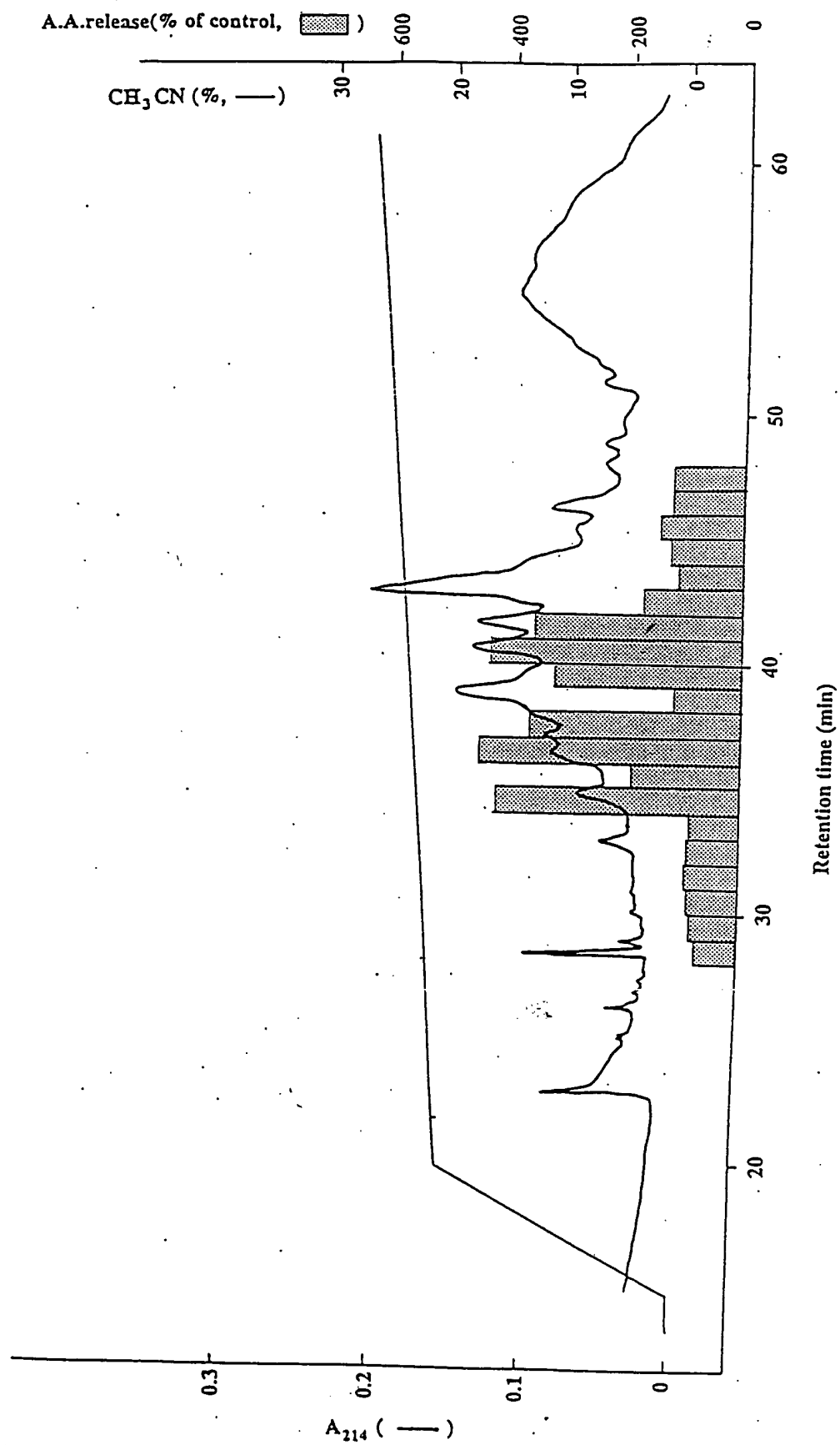
Fig. 17



bovine hypothalamus extract

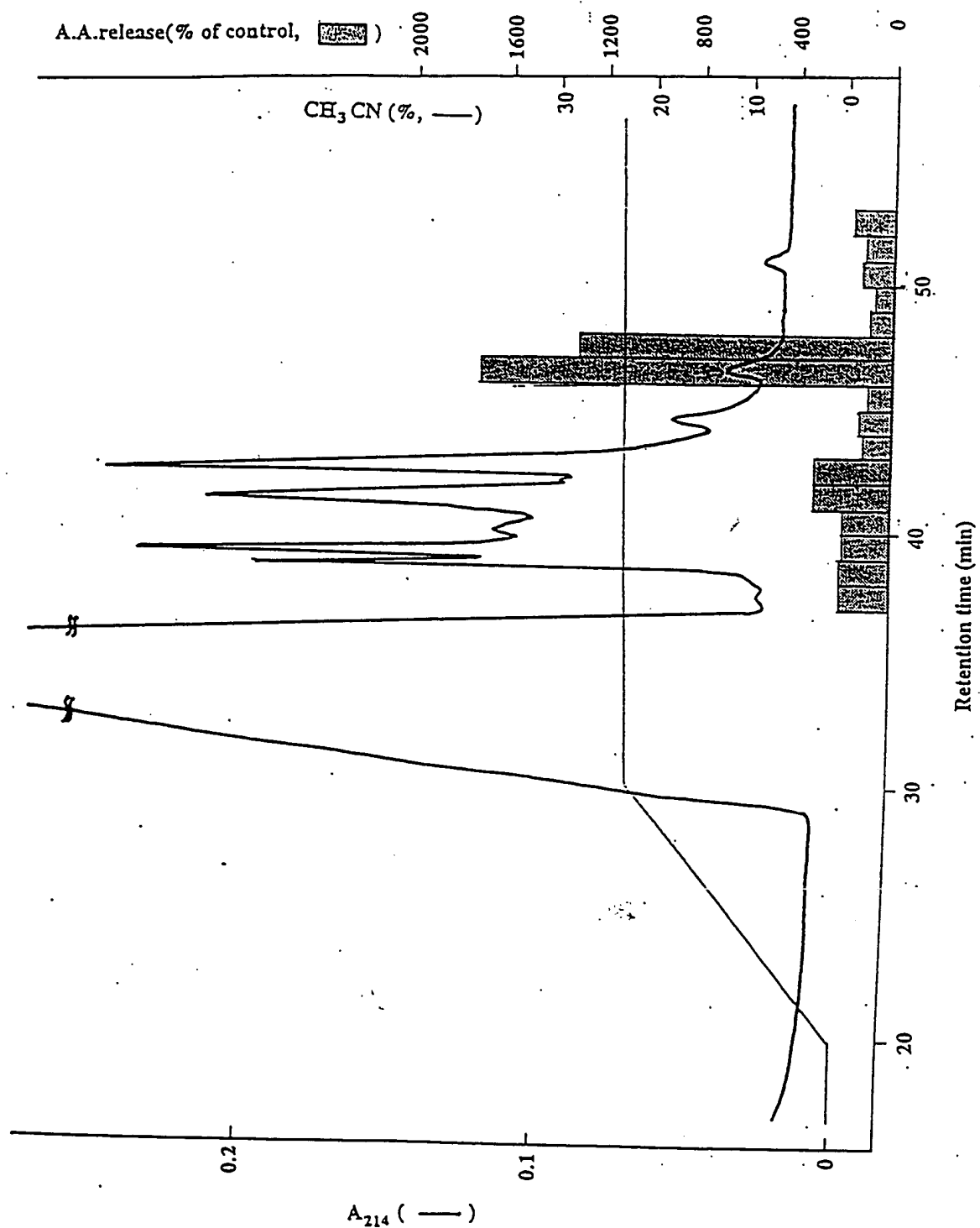
C₁₈-column CH₃CN elution (%)

Fig. 1



19/53

Fig. 19



0002250" 06292560

Fig. 20

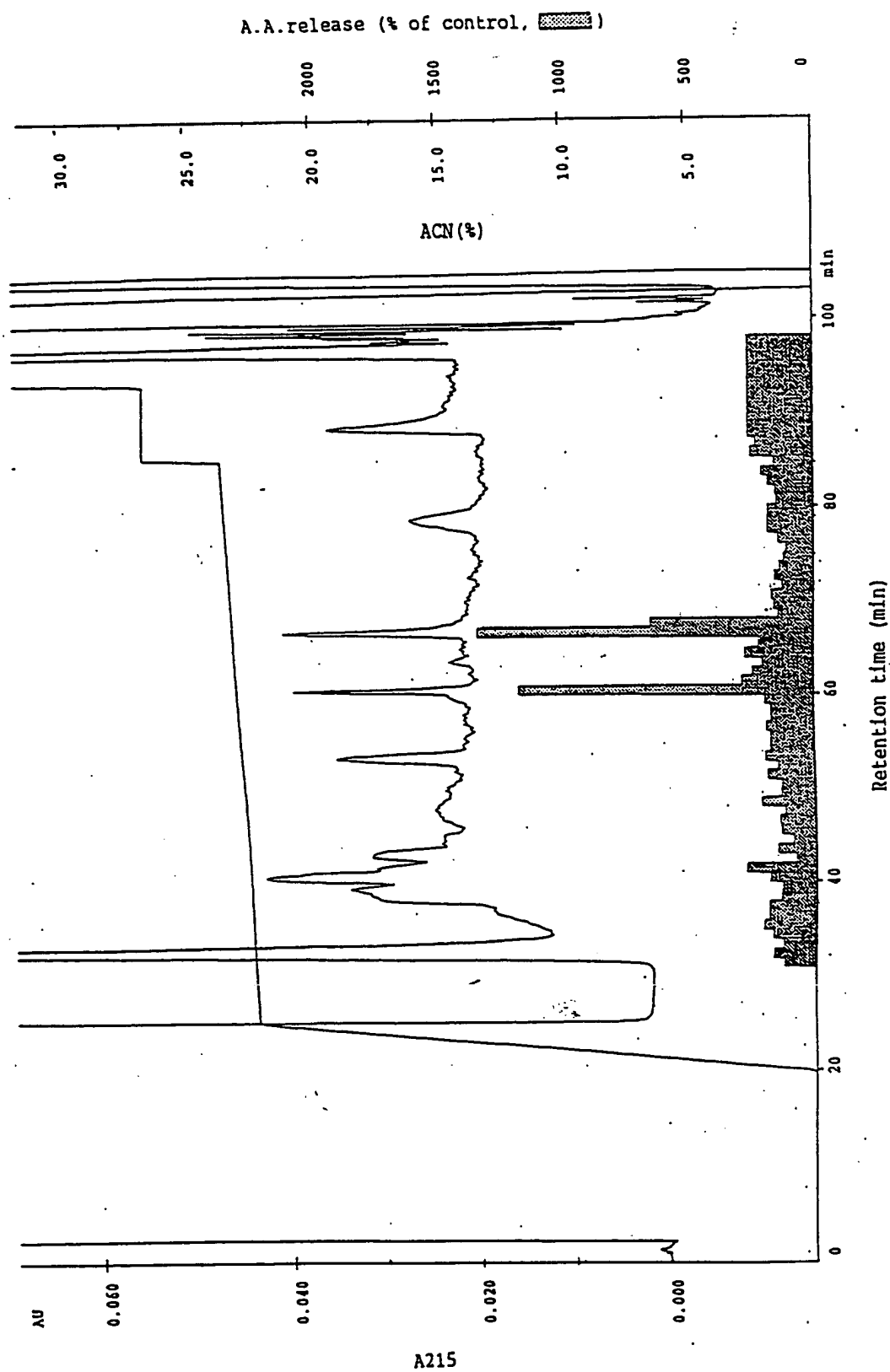
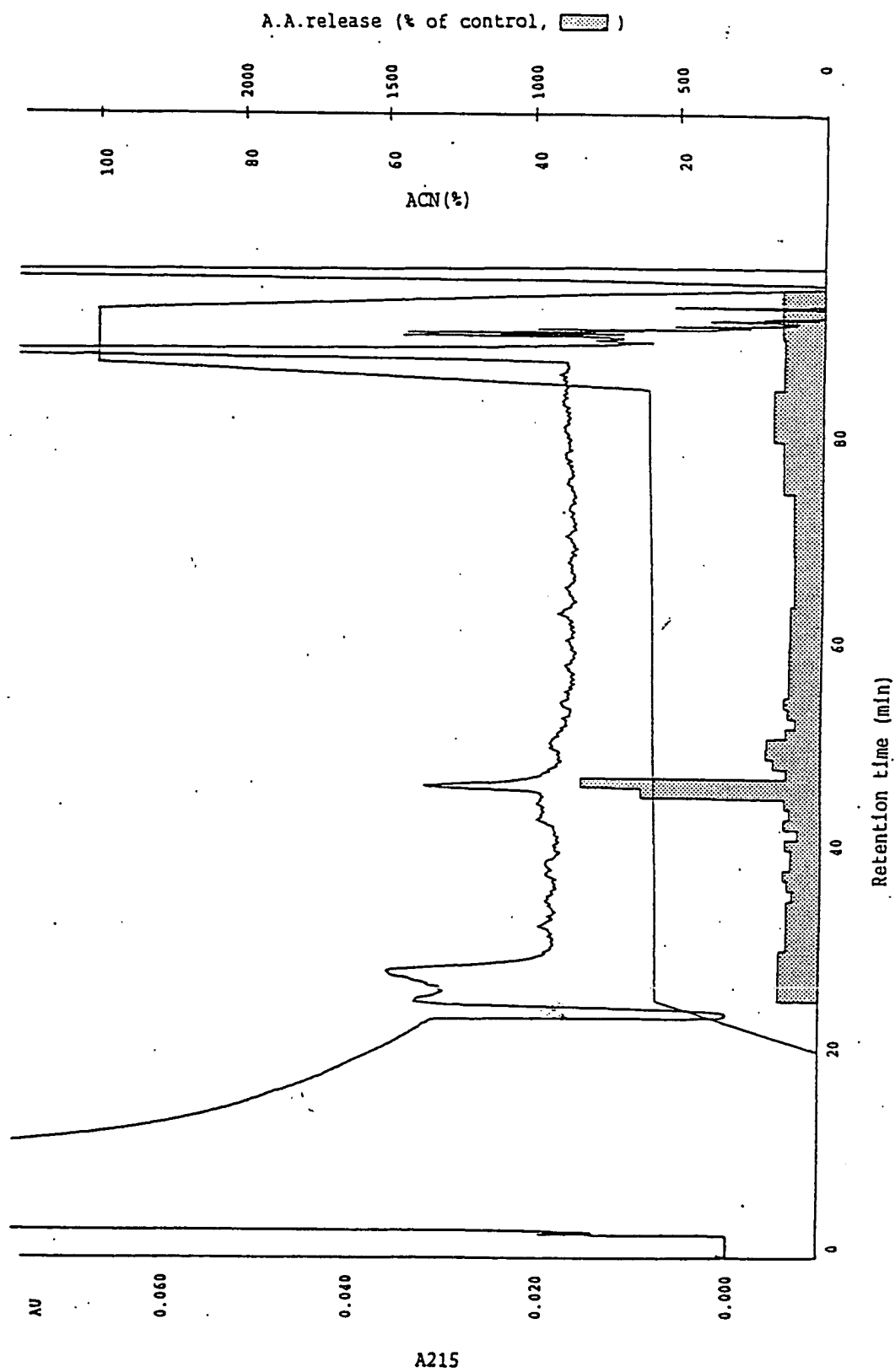


Fig. 21



```

P5-1
5'  GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr
    9      18      27      36      45      54
    GCG GGC CGT GGG ATC CGG CCC G 3'
    --- --- --- --- --- --- ---
    Ala Gly Arg Gly Ile Arg Pro
P3-2

```

Fig. 23

| | | |
|-----|--|-----|
| 1 | GTGGAATGAAGGCGGTGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG | 59 |
| 1 | MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu | 18 |
| 60 | CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCGACATCAAC | 119 |
| 19 | GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn | 38 |
| | ← PDN | |
| 120 | CCTGCCT | 126 |
| 39 | <u>ProAla</u> | 40 |

006250 0529660

Fig. 24(a)

| | | |
|-----|---|-----|
| 1 | GTGGAATGAAGCGGTGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCTGGCCCTG | 59 |
| 1 | MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu | 18 |
| 60 | CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCGACATCAAC | 119 |
| 19 | GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn | 38 |
| 120 | CCTGCCTGGTACGCRGGCCCGTGGGATCCGGCCCGTGGGCCGCTTCGGCCGGCGAAGAGCT | 179 |
| 39 | ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla | 58 |
| 180 | GCCCCGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA | 239 |
| 59 | AlaProGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu | 78 |
| 240 | GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCCAGCTGGTCCAGGAA | 299 |
| 79 | GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu | 98 |
| 300 | TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCTCT | 359 |
| 98 | | 98 |
| 360 | AATAAAAGCAGCTGGCTTGTT | 380 |
| 98 | | 98 |

| | | |
|-----|---|-----|
| 1 | GTGGAATGAAGCGGTGGGGGCGCTGCCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG | 59 |
| 1 | MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu | 18 |
| 60 | CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC | 119 |
| 19 | GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn | 38 |
| 120 | CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCCGTGGGCCGCTTCGGCCGGCGAAGAGCT | 179 |
| 39 | ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgAla | 58 |
| 180 | GCCCTGGGGGACGGACCCAGGCCCTGGCCCCCGCGCTGTGCCGGCCTGCTTCCGCCTGGAA | 239 |
| 59 | AlaLeuGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu | 78 |
| 240 | GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCCAGCTGGTCCAGGAA | 299 |
| 79 | GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu | 98 |
| 300 | TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT | 359 |
| 98 | | 98 |
| 360 | AATAAAAGCAGCTGGCTTGT | 380 |
| 98 | | 98 |

Fig. 25

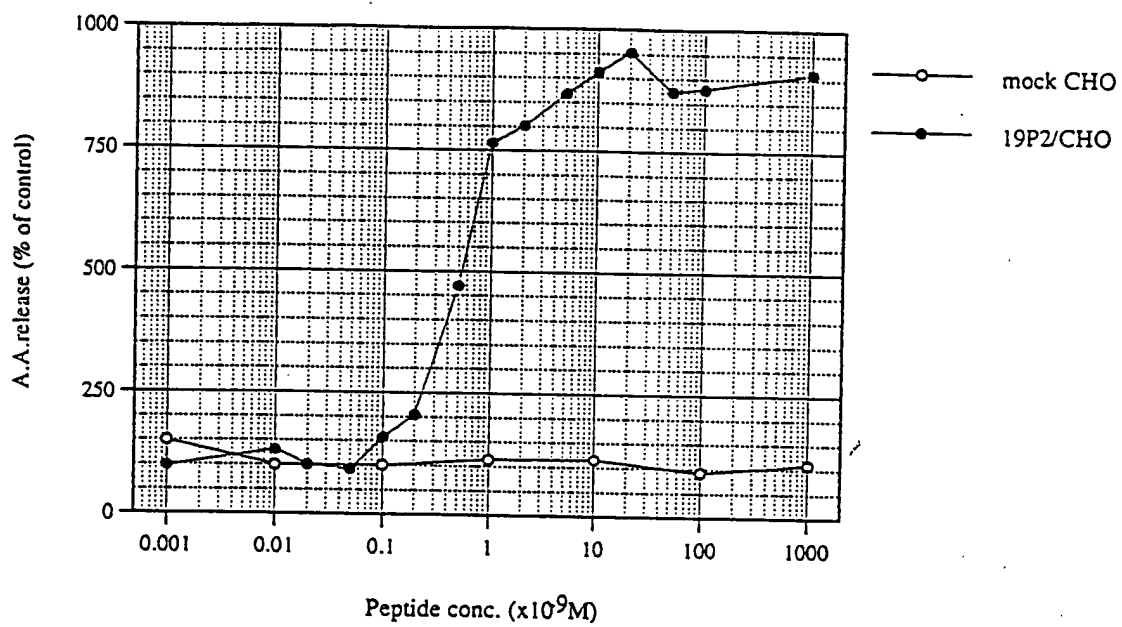


Fig. 26

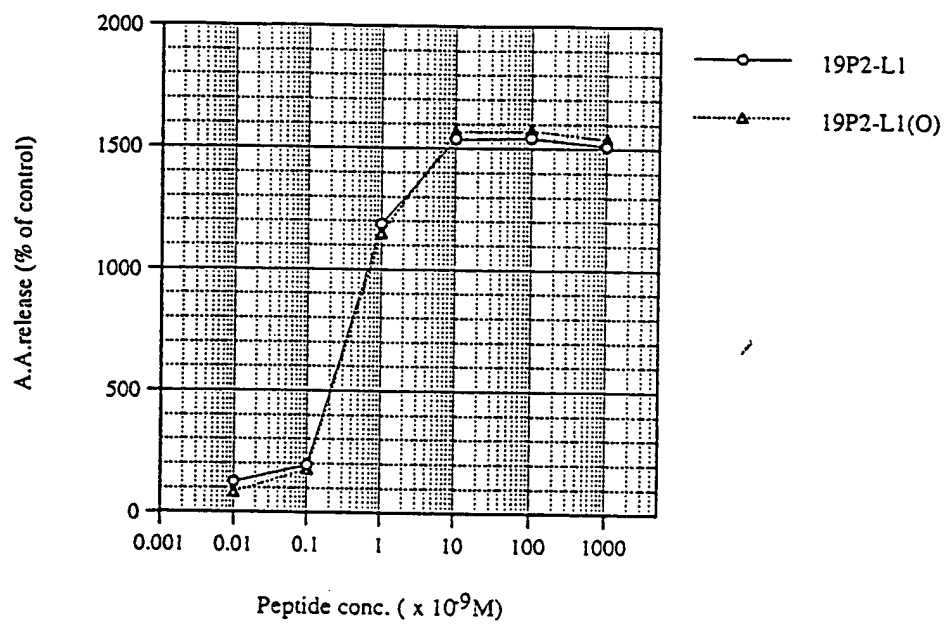


Fig. 27

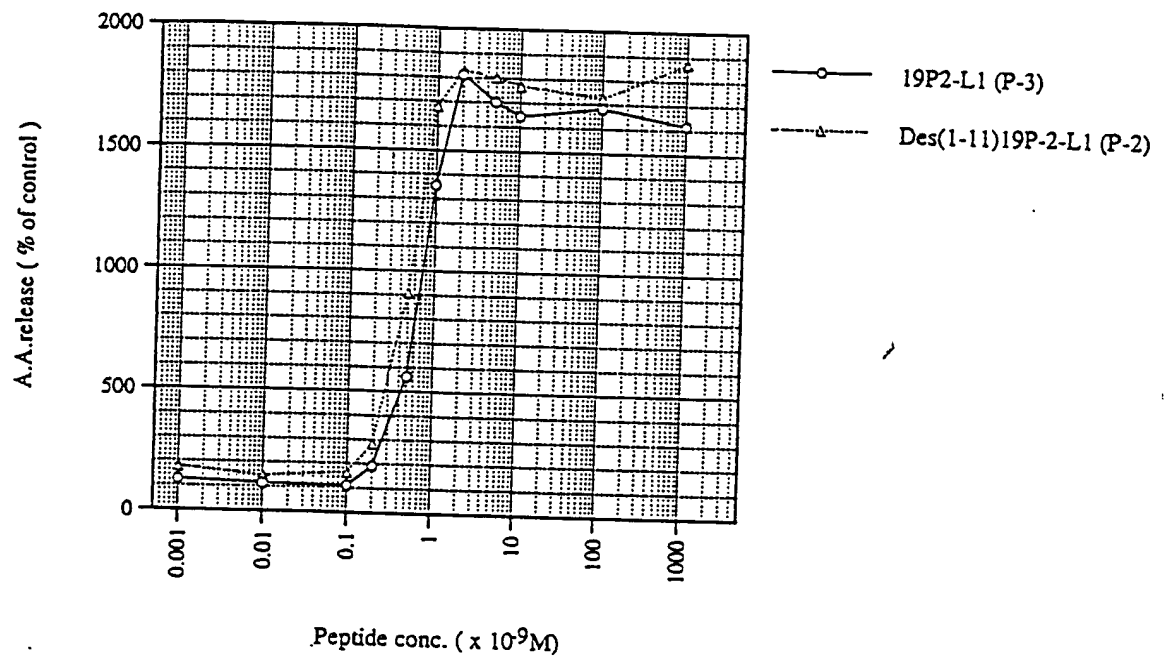
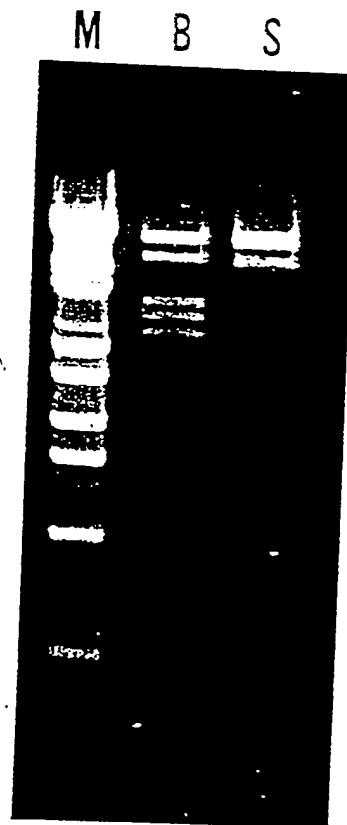


Fig. 28



006250 0529650

Fig. 29

| | | | | | |
|------------|-------------|------------|------------|-------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| ATGAAGGCGG | TGGGGGCCTG | GCTCCTCTGC | CTGCTGCTGC | TGGGCCTGGC | CCTGCAGGGG |
| 70 | 80 | 90 | 100 | 110 | 120 |
| GCTGCCAGCA | GAGCCACCA | GCACTCCATG | GAGATCCGCA | GTGAGTGTCT | AGCCCCGCCC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| CTGCCCCCAG | GGGTCACAGG | GGGGGCCTGG | CCACTTCCTG | GGCTGGGACA | TCCTTGCTAA |
| 190 | 200 | 210 | 220 | 230 | 240 |
| GCATCCTGGG | GTTGGGGTTT | GGCCTCCTGT | TCCCCAGACC | CTTCCCCCAG | GTGGCCCGGA |
| 250 | 260 | 270 | 280 | 290 | 300 |
| CAGGTGCTCC | CAAGGGTCCC | GGCCCAGCAC | ACGGGGGAGG | GTCACCTCCTC | ACCACACGGG |
| 310 | 320 | 330 | 340 | 350 | 360 |
| TGGCCTGGGG | CTGAGTGCAC | GTCACCCATG | AGAACGGGGC | TGTGAGGACA | GGAAAGGAAG |
| 370 | 380 | 390 | 400 | 410 | 420 |
| GGGAGTGTGT | CCTGGTGTGA | GTCTGAAATC | CTACTTCCCA | AAGCCACCCC | AGCACCAGAA |
| 430 | 440 | 450 | 460 | 470 | 480 |
| ATGGGCGCTC | CGGGTGAACC | TCCTGTGCGG | GTGGGTGGTC | CTGGCATGGC | CTGGGCGACA |
| 490 | 500 | 510 | 520 | 530 | 540 |
| GGCAGCCATG | AGCTGAGCAC | ACACCCGGCC | CGGCCACCAG | GGCTGTATGC | TCCAGGGCAC |
| 550 | 560 | 570 | 580 | 590 | 600 |
| AGGCCTCCAT | GCGCTCTTCT | CTCTCTTTCC | AGCCCCGAC | ATCAACCCTG | CCTGGTACGG |
| 610 | 620 | 630 | 640 | 650 | 660 |
| AGGCCGTGGG | ATCCGGCCCCG | TGGGCCGCTT | CGGCCGGCGA | AGAGCTGCCC | TGGGGGACGG |
| 670 | 680 | 690 | 700 | 710 | 720 |
| ACCCAGGCCT | GGCCCCCGGC | GTGTGCCGGC | CTGCTCCGC | CTGAAGGCG | GTGCTGAGCC |
| 730 | 740 | 750 | 760 | 770 | 780 |
| CTCCCGAGCC | CTCCCGGGGC | GGCTGACGGC | CCAGCTGGTC | CAGGAATAA. | |

0527690-052300

Fig. 30

| | | | | | | |
|--------|----------------|------------|------------|-------------|------------|-----|
| genome | 10 | 20 | 30 | 40 | 50 | |
| cDNA | 1 ATGAAGGCGG | TGGGGGCTG | GCTCCTCTGC | CTGCTGCTGC | TGGGCCTGGC | 50 |
| | 1 ATGAAGGCGG | TGGGGGCTG | GCTCCTCTGC | CTGCTGCTGC | TGGGCCTGGC | 50 |
| genome | 60 | 70 | 80 | 90 | 100 | |
| cDNA | 51 CCTGCAGGGG | GCTGCCAGCA | GAGCCCACCA | GCACTCCATG | GAGATCCGCA | 100 |
| | 51 CCTGCAGGGG | GCTGCCAGCA | GAGCCCACCA | GCACTCCATG | GAGATCCGCA | 100 |
| genome | 110 | 120 | 130 | 140 | 150 | |
| cDNA | 101 GTGAGTGTCT | AGCCCCGCCC | CTGCCCCCAG | GGGTACAGG | GGGGGCTGG | 150 |
| | 101 ----- | ----- | ----- | ----- | ----- | 150 |
| genome | 160 | 170 | 180 | 190 | 200 | |
| cDNA | 151 CCACTTCCTG | GGCTGGGACA | TCCTMGCTAA | GCATCCTGGG | GTTGGGGTTT | 200 |
| | 151 ----- | ----- | ----- | ----- | ----- | 200 |
| genome | 210 | 220 | 230 | 240 | 250 | |
| cDNA | 201 GGCCTCCTGT | TCCCCAGACC | CTTCCCCCAG | GTGGCCCCGA | CAGGTGCTCC | 250 |
| | 201 ----- | ----- | ----- | ----- | ----- | 250 |
| genome | 260 | 270 | 280 | 290 | 300 | |
| cDNA | 251 CAAGGGTCCC | GGCCCAGCAC | ACGGGGGAGG | GTCACCTCTC | ACCACACGGG | 300 |
| | 251 ----- | ----- | ----- | ----- | ----- | 300 |
| genome | 310 | 320 | 330 | 340 | 350 | |
| cDNA | 301 TGGCCTGGGG | CTGAGTGCAC | GTCACCCATG | AGAACGGGGC | TGTGAGGACA | 350 |
| | 301 ----- | ----- | ----- | ----- | ----- | 350 |
| genome | 360 | 370 | 380 | 390 | 400 | |
| cDNA | 351 GGAAAGGAAG | GGGAGTGTGT | CCTGGTGTGA | GTCTGAAATC | CTACTTCCCA | 400 |
| | 351 ----- | ----- | ----- | ----- | ----- | 400 |
| genome | 410 | 420 | 430 | 440 | 450 | |
| cDNA | 401 AAGCCACCCC | AGCACCAGAA | ATGGGCGCTC | CGGGTGAACC | TCCTGTGCGG | 450 |
| | 401 ----- | ----- | ----- | ----- | ----- | 450 |
| genome | 460 | 470 | 480 | 490 | 500 | |
| cDNA | 451 GTGGGTGGTC | CTGGCATGGC | CTGGGCGACA | GGCAGCCATG | AGCTGAGCAC | 500 |
| | 451 ----- | ----- | ----- | ----- | ----- | 500 |
| genome | 510 | 520 | 530 | 540 | 550 | |
| cDNA | 501 ACACCCGGCC | CGGCCACCAG | GGCTGTATGC | TCCAGGGCAC | AGGCCTCCAT | 550 |
| | 501 ----- | ----- | ----- | ----- | ----- | 550 |
| genome | 560 | 570 | 580 | 590 | 600 | |
| cDNA | 551 GCGCTCTTCT | CTCTCTTTTC | AGCCCCCGAC | ATCAACCCCTG | CCTGGTACGC | 600 |
| | 551 ----- | ----- | ----- | ----- | ----- | 600 |
| genome | 610 | 620 | 630 | 640 | 650 | |
| cDNA | 601 AGGCCGTGGG | ATCCGGCCCG | TGGGCGGCTT | CGGCCGGCGA | AGAGCTGCCC | 650 |
| | 601 GGGCCGTGGG | ATCCGGCCCG | TGGGCGGCTT | CGGCCGGCGA | AGAGCTGCCC | 650 |
| genome | 660 | 670 | 680 | 690 | 700 | |
| cDNA | 651 TGGGGGACGG | ACCCAGGCCT | GGCCCCCGGC | GTGTGCCGGC | CTGCTTCCGC | 700 |
| | 651 CGGGGGACGG | ACCCAGGCCT | GGCCCCCGGC | GTGTGCCGGC | CTGCTTCCGC | 700 |
| genome | 710 | 720 | 730 | 740 | 750 | |
| cDNA | 701 CTGGAAGGCG | GTGCTGAGCC | CTCCCGAGCC | CTCCCGGGGC | GGCTGACGGC | 750 |
| | 701 CTGGAAGGCG | GTGCTGAGCC | CTCCCGAGCC | CTCCCGGGGC | GGCTGACGGC | 750 |
| genome | 760 | 770 | 780 | 790 | 800 | |
| cDNA | 751 CCAGCTGGTC | CAGGAATAA. | | | | 800 |
| | 751 CCAGCTGGTC | CAGGAATAA. | | | | 800 |

09576250-052300

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 5' | 9 | | | 18 | | | 27 | | | 36 | | | 45 | | | 54 | | |
| ATG | AAG | GCG | GTG | GGG | GCC | TGG | CTC | CTC | TGC | CTG | CTG | CTG | CTG | GGC | CTG | GCC | CTG | |
| M | K | A | V | G | A | W | L | L | C | L | L | L | L | G | L | A | L | |
| 63 | | | 72 | | | 81 | | | 90 | | | 99 | | | 108 | | | |
| CAG | GGG | GCT | GCC | AGC | AGA | GCC | CAC | CAG | CAC | TCC | ATG | GAG | ATC | CGC | ACC | CCC | GAC | |
| Q | G | A | A | S | R | A | H | Q | H | S | M | E | I | R | T | P | D | |
| 117 | | | 126 | | | 135 | | | 144 | | | 153 | | | 162 | | | |
| ATC | AAC | CCT | GCC | TGG | TAC | GCA | GGC | CGT | GGG | ATC | CGG | CCC | GTG | GGC | CGC | TTC | GGC | |
| I | N | P | A | W | Y | A | G | R | G | I | R | P | V | G | R | F | G | |
| 171 | | | 180 | | | 189 | | | 198 | | | 207 | | | 216 | | | |
| CGG | CGA | AGA | GCT | GCC | CTG | GGG | GAC | GGA | CCC | AGG | CCT | GGC | CCC | CGG | CGT | GTG | CCG | |
| R | R | R | A | A | L | G | D | G | P | R | P | G | P | R | R | V | P | |
| 225 | | | 234 | | | 243 | | | 252 | | | 261 | | | 270 | | | |
| GCC | TGC | TTC | CGC | CTG | GAA | GGC | GGT | GCT | GAG | CCC | TCC | CGA | GCC | CTC | CCG | GGG | CGG | |
| A | C | F | R | L | E | G | G | A | E | P | S | R | A | L | P | G | R | |
| 279 | | | 288 | | | 297 | | | | | | | | | | | | |
| CTG | ACG | GCC | CAG | CTG | GTC | CAG | GAA | TAA | 3' | | | | | | | | | |
| L | T | A | Q | L | V | Q | E | * | | | | | | | | | | |

| | | |
|-----|---|-----|
| 1 | GGCATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTTGCTGCTG | 59 |
| 1 | MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu | 12 |
| 60 | CTAAGCTTGGTCCTCCCAGGGGCTTCCAGCCGAGCCCACCAGCACTCCATGGAGACAAGA | 119 |
| 13 | LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg | 32 |
| 120 | ACCCCTGATATCAATCCTGCCTGGTACACGGGCCGCGGGATCAGGCCTGTGGGCCGCTTC | 179 |
| 33 | ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe | 52 |
| 180 | GGCAGGAGAAGGGCAACCCCCAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCTCCCA | 239 |
| 53 | GlyArgArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro | 72 |
| 240 | CTGGATGGACGCACCAAGTTCTCTCAGCGTGGATAACACCCCAGCTCGAGAAGACAGTGC | 299 |
| 73 | LeuAspGlyArgThrLysPheSerGlnArgGly*** | 83 |
| 300 | TGCTGAGCCCCAAGCCCACACTCCCTGTCCCCTGCAGACCCTCCTCTACCCTCCCTCTCCT | 359 |
| 83 | | 83 |
| 360 | CTGCT | 364 |
| 83 | | 83 |

| | | | | | | |
|------------|-----------|-----------------------------------|---------------|-------------------|------------|-------------|
| bovine.aa | | | | M K A V G A W L L | | |
| | | 10 | 20 | 30 | 40 | 50 |
| bovine.seq | -18 |GT | GGAATGAAGG | CGGTGGGGGC | CTGGCTCCTC | |
| rat.seq | 1 | GGCATCATCC | AGGAAGACGG | AGCATG---G | CCTGAAGAC | GTGGCTTCTG |
| bovine.aa | | C L L L L G L A L Q | G A A S R A H | | | |
| | | 60 | 70 | 80 | 90 | 100 |
| bovine.seq | 33 | TGCCTGTGTC | TGCTGGGCCT | GCCCCTGCAG | GGGGCTGCCA | GCAGAGCCCCA |
| rat.seq | 51 | TGCTTGCTGC | TGCTAAGCTT | GGTCTCTCCA | GGGGCTTCCA | GCAGAGCCCCA |
| | | | R1 | | | |
| bovine.aa | | Q H S M E I R T P D I N P A W Y A | | | | |
| | | 110 | 120 | 130 | 140 | 150 |
| bovine.seq | 83 | CCAGCACTCC | ATGGAGATCC | GCACCCCGCA | CATCAACCCT | GCCTGGTAGC |
| rat.seq | 101 | CCAGCACTCC | ATGGAGACAA | GAACCCCTGA | TATCAATCT | GCCTGGTAGC |
| | | | | | R3 | |
| bovine.aa | | G R G I R P V G R F G R R R A A | | | | |
| | | 160 | 170 | 180 | 190 | 200 |
| bovine.seq | 133 | CGGGCCGTGG | GATCCGGCCC | GTGGGCGCGT | TCGGCCCGGG | AAGAGCTGCC |
| rat.seq | 151 | CGGGCCCGCG | GATCAGGCCT | GTGGGCGCGT | TCGGCAGGAG | AAGGGCAACC |
| | | | | R4 | | |
| bovine.aa | | P G D G P R P G P R R V P A C F R | | | | |
| | | 210 | 220 | 230 | 240 | 250 |
| bovine.seq | 183 | CCGGGGGACG | GACCCAGGCC | TGGCCCCCGG | CGTGTGCCGG | CCTGCTTCCG |
| rat.seq | 201 | CCGAGGGATG | TCACTGGACT | TGGC----- | ---CAACTCA | GCTGCCTCCC |
| bovine.aa | | L E G G A E P S R A L P G R L T A | | | | |
| | | 260 | 270 | 280 | 290 | 300 |
| bovine.seq | 233 | CCTGGAAGGC | GGCGTGAGC | CCTCCCGAGC | CCTCCCGGGG | CGGCTGACGG |
| rat.seq | 251 | ACTGGATGGA | CGCACCAAGT | TCTCTCAGCG | TGGATAACAC | CCCAGCTCGA |
| bovine.aa | | Q L V Q E * | | | | |
| | | 310 | 320 | 330 | 340 | 350 |
| bovine.seq | 283 | CCCAGCTGGT | CCAGGAATAA | CAGCGGGAGC | CTGCCCCCCA | CCCTCTCTCC |
| rat.seq | 301 | GAAGACAGTG | CTGCTGAGCC | CAAGCCCA | CTCCCTGTCC | CCTGCAGACC |
| bovine.aa | | | | | | |
| | | 360 | 370 | 380 | 390 | 400 |
| bovine.seq | 333 | TCCACCAGCC | ACCTTCCCTC | CAGTCCTAAT | AAAAGCAGCT | GGCTTGTT.. |
| rat.seq | 351 | CTCCTCTACC | CTCCCTCTCC | TCTGCT.... | | |

Fig. 34

| | | |
|-----|---|-----|
| 1 | GGCCTCCTCGGAGGAGCCAAGGGATGAAGGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG | 59 |
| 1 | MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu | 12 |
| 60 | ATGCTGGGCCTGGCCCTGCGGGGAGCTGCAAGTCGTACCCATCGGCACTCCATGGAGATC | 119 |
| 13 | MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle | 32 |
| 120 | CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCTGTGGGCCCGC | 179 |
| 33 | ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg | 52 |
| 180 | TTCGGTCGGAGGAGGGCAACCCTGGGGGACGTCCCCAAGCCTGGCCTGCGACCCCGGCTG | 239 |
| 53 | PheGlyArgArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu | 72 |
| 240 | ACCTGCTTCCCCCTGGAAGGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCTTGT | 299 |
| 73 | ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly*** | 87 |
| 300 | CAAGAACTCACTCTGGAGCCTCCCCCACCACCCCTCTCCTCTCCTTCGGGGCTCCTTTC | 359 |
| 87 | | 87 |
| 360 | CC | 361 |
| 87 | | 87 |

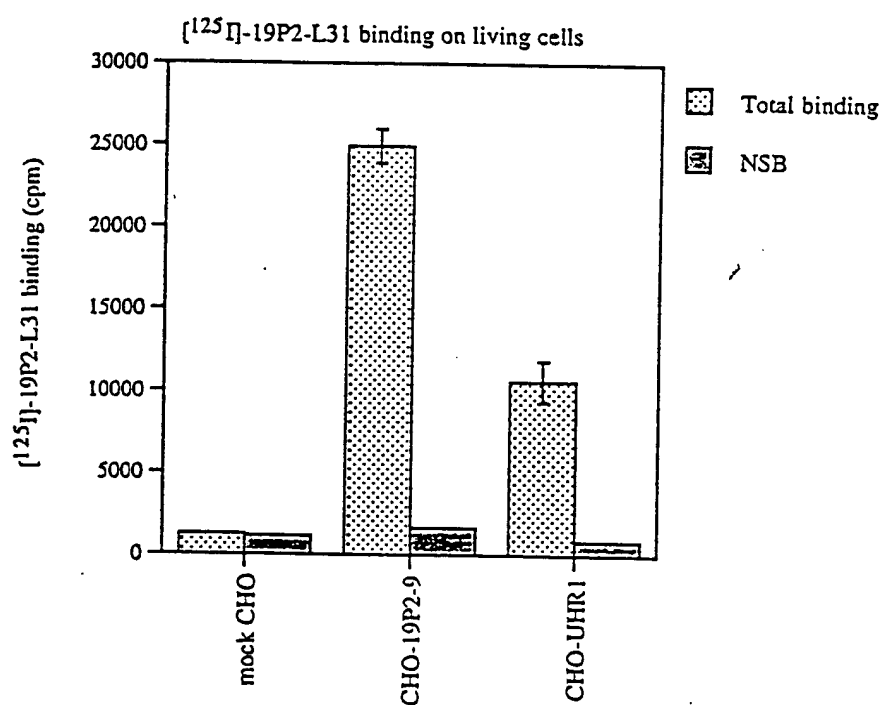
00576250 052300

Fig. 35

| | | | | | | |
|-----------|---------------|------------|------------|------------|------------|-----|
| | 10 | 20 | 30 | 40 | 50 | |
| bovine.aa | 1 MKAVGAWLLC | LLLLGLALQG | AASRAHQHSM | EIRTPDINPA | WYAGRGIREV | 50 |
| rat.aa | 1 M-ALKTWLLC | LLLLSLVLPQ | ASSRAHQHSM | ETRTPDINPA | WYTGRGIREV | 50 |
| human.aa | 1 MKVLRAWLLC | LLMLGLALRG | AASRTHRHSM | EIRTPDINPA | WYASRGIREV | 50 |
| | 60 | 70 | 80 | 90 | 100 | |
| bovine.aa | 51 GRFGRRRAAP | GDCFRFGPRR | VPACFRLEGG | AEPSRALPGR | LTAQLVQE* | 100 |
| rat.aa | 51 GRFGRRRATP | RDVTGLG--- | QLSCLPLDGR | TKFSQRG*.. | | 100 |
| human.aa | 51 GRFGRRRATL | GDVFKPGLRP | RLTCFPLEGG | AMSSQDG*.. | | 100 |

00576290.052300

Fig. 36



cells; 0.5×10^7 cells/ml

[¹²⁵I]-19P2-L31; 200pM (avg. 63857.3cpm)

NSB; 200nM (x 1,000)

reaction; RT, 2.5hr

in HBSS + 0.05% BSA + 0.05% CHAPS
in 100 μ l

Fig. 37

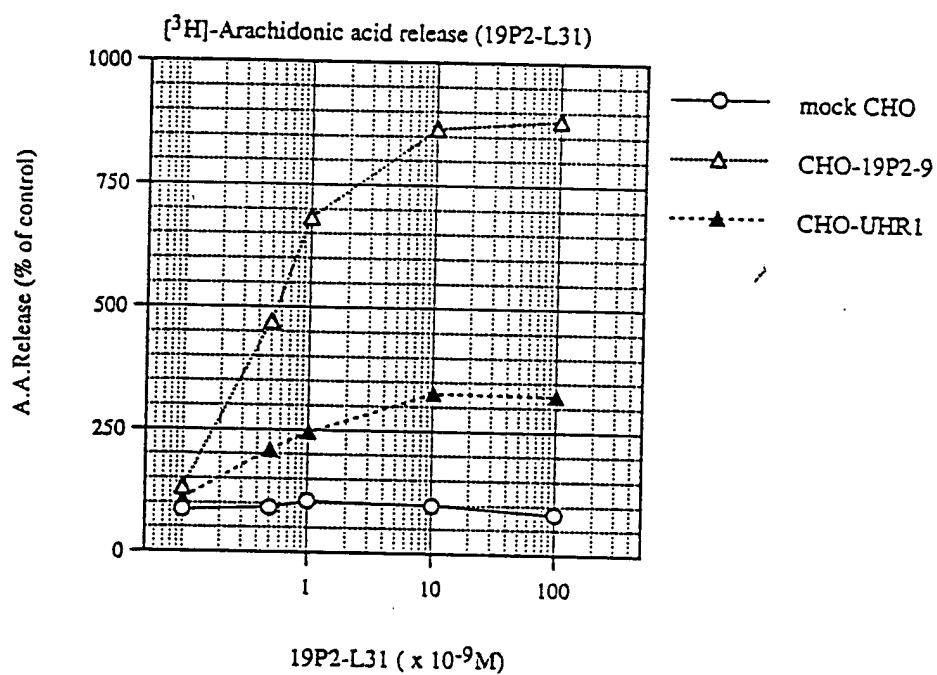
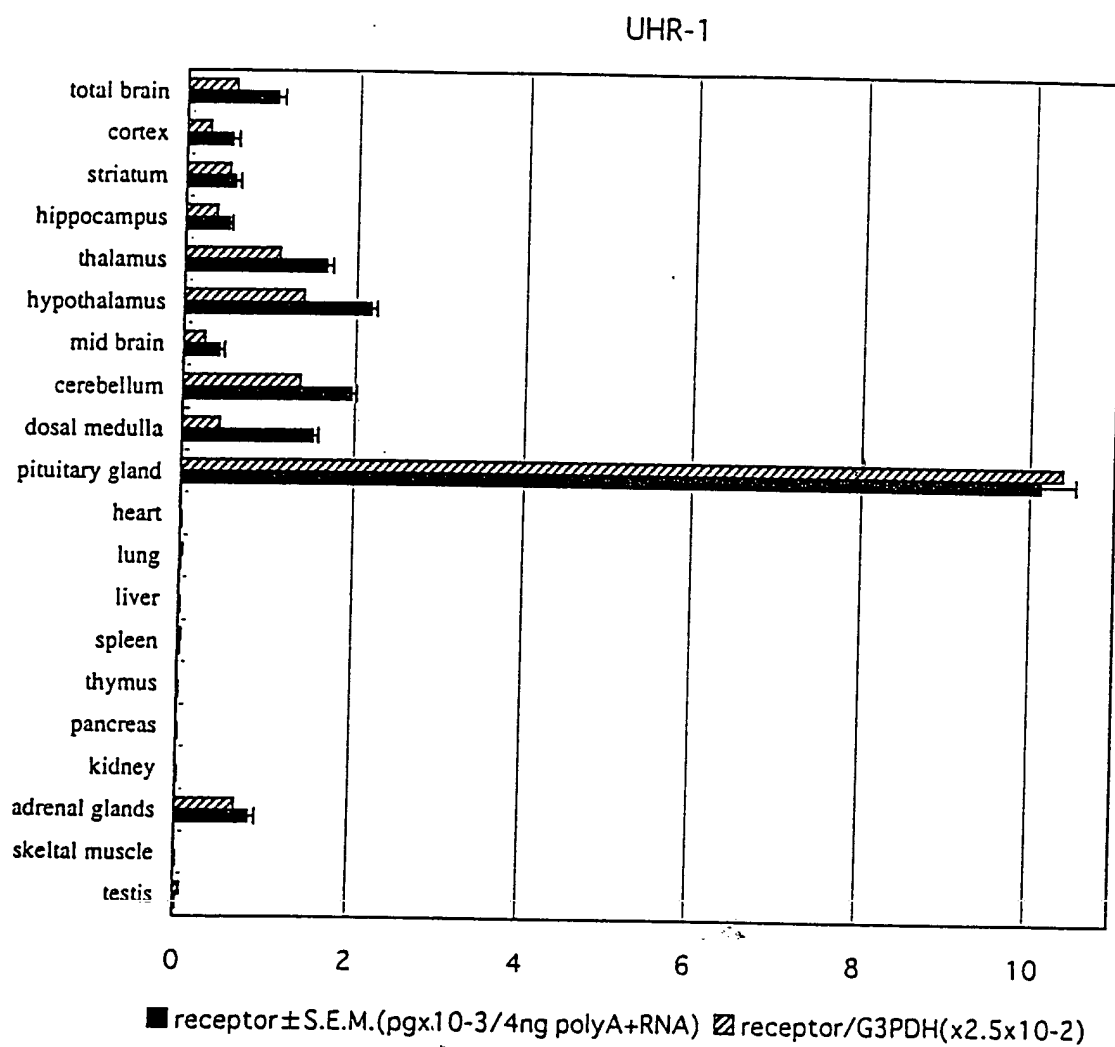


Fig. 38



006340" 0629/86

Fig. 39

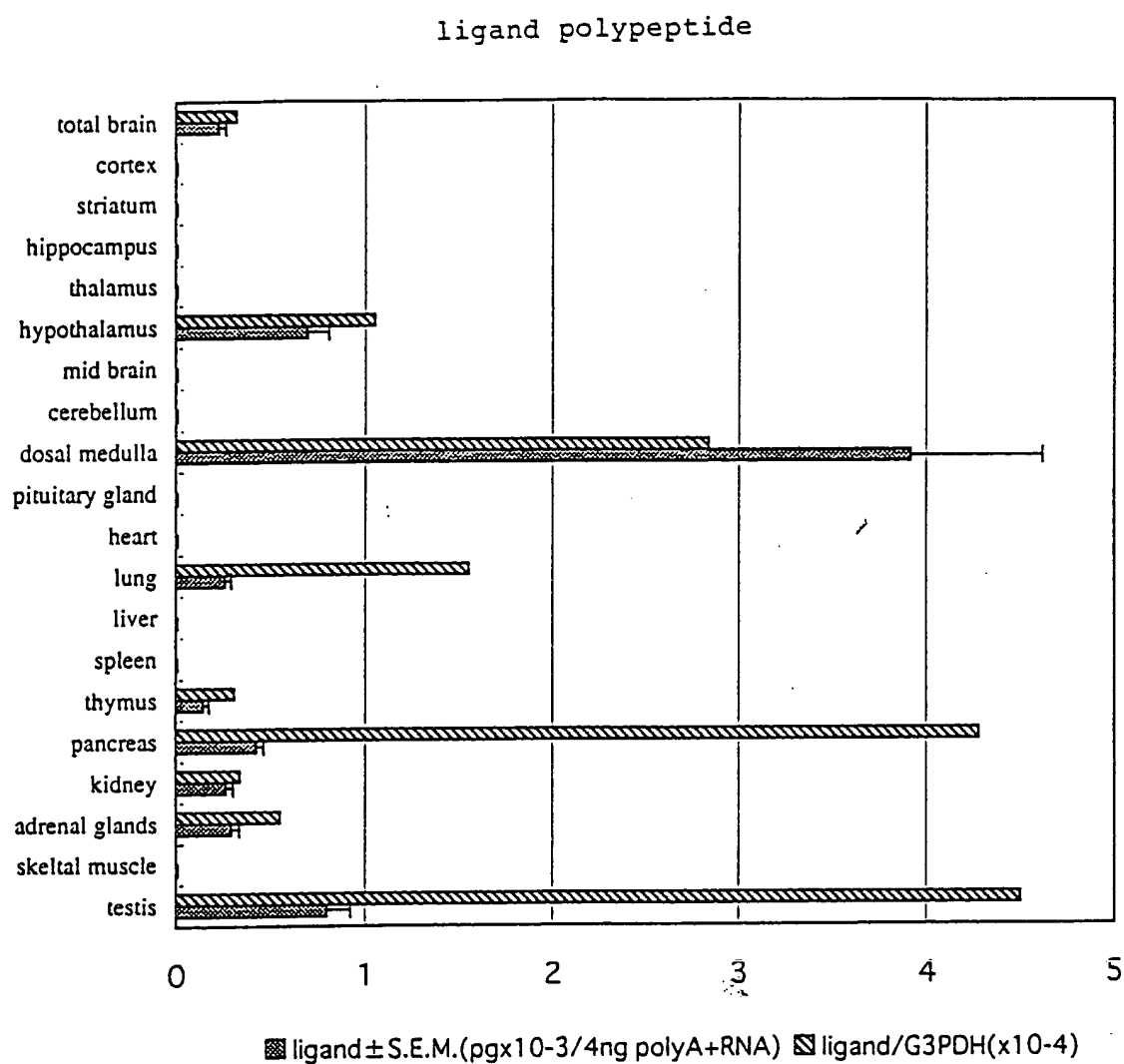


Fig. 40

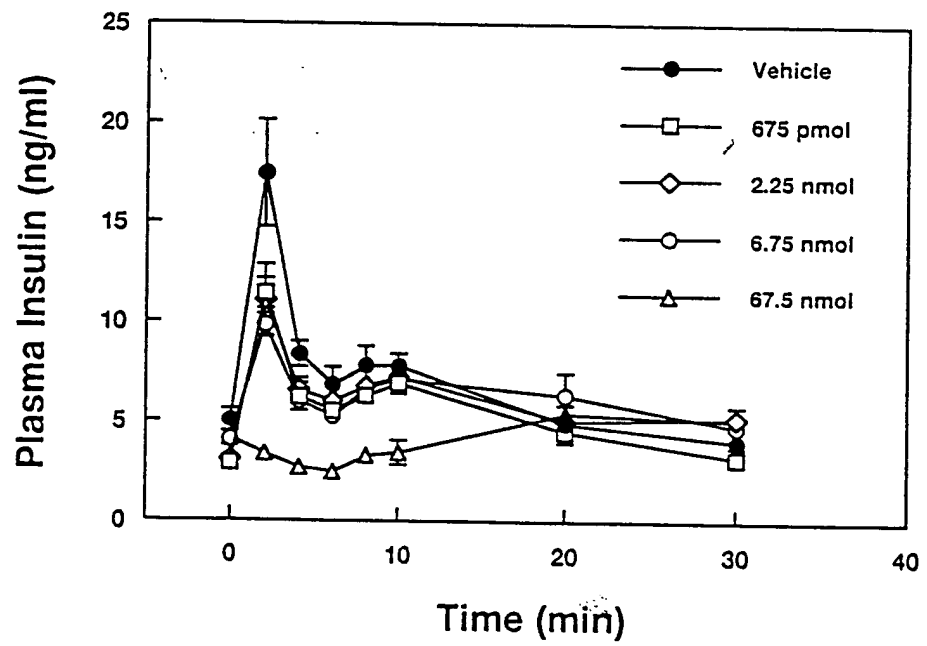
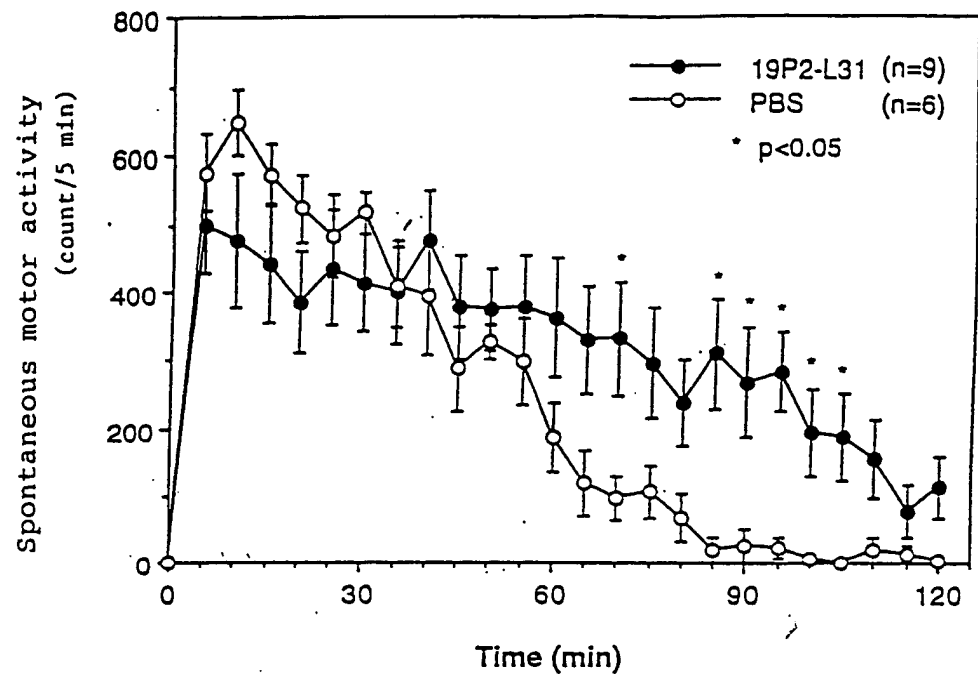


Fig. 41

(a)



(b)

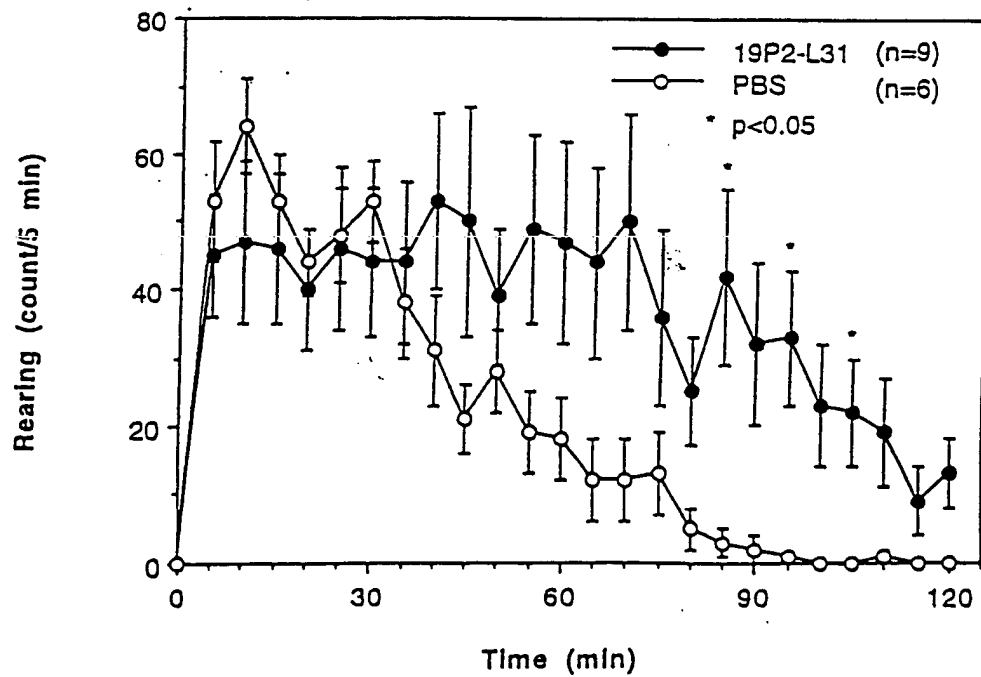
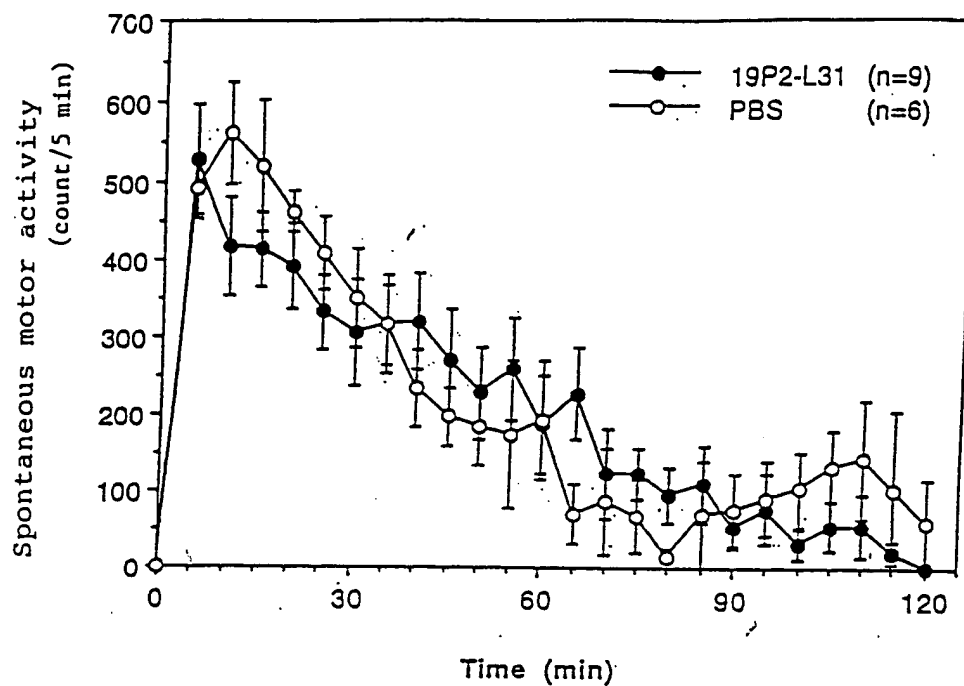


Fig. 42

(a)



(b)

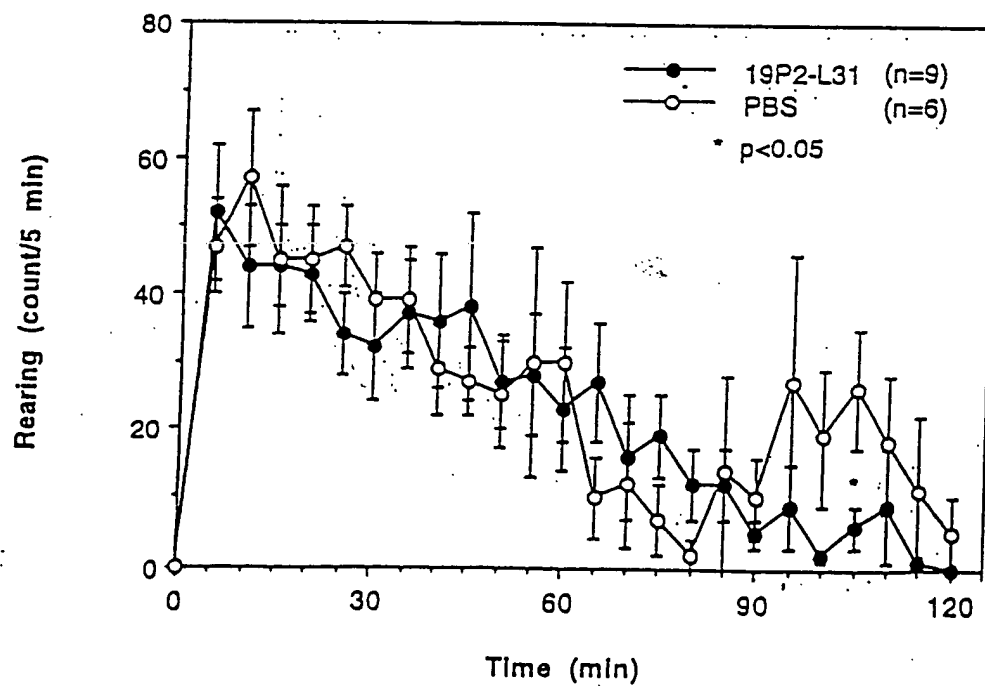
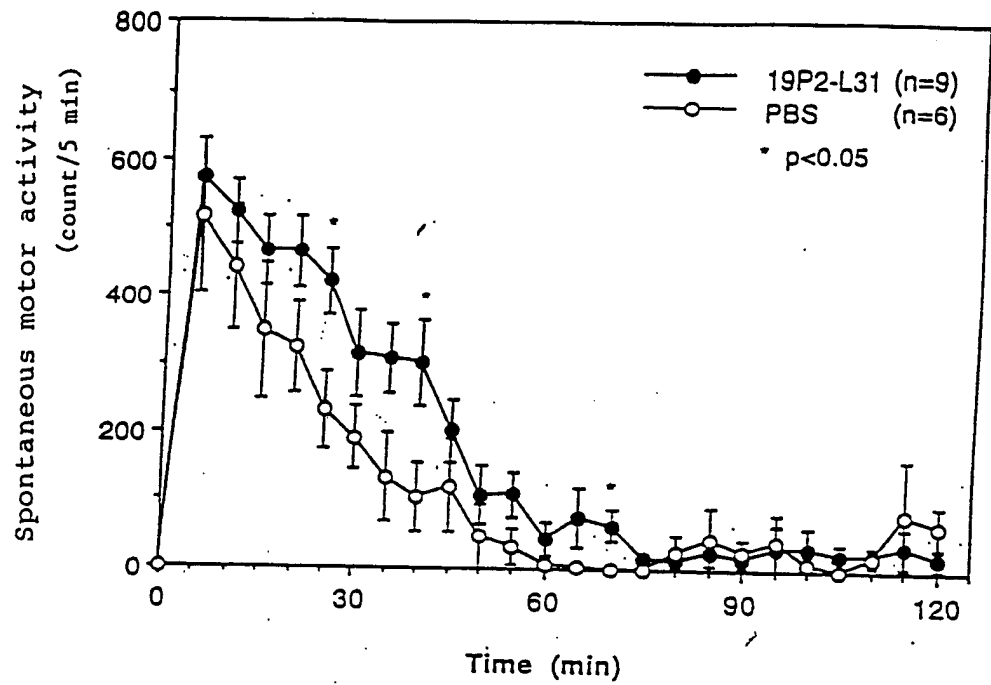


Fig. 43

(a)



(b)

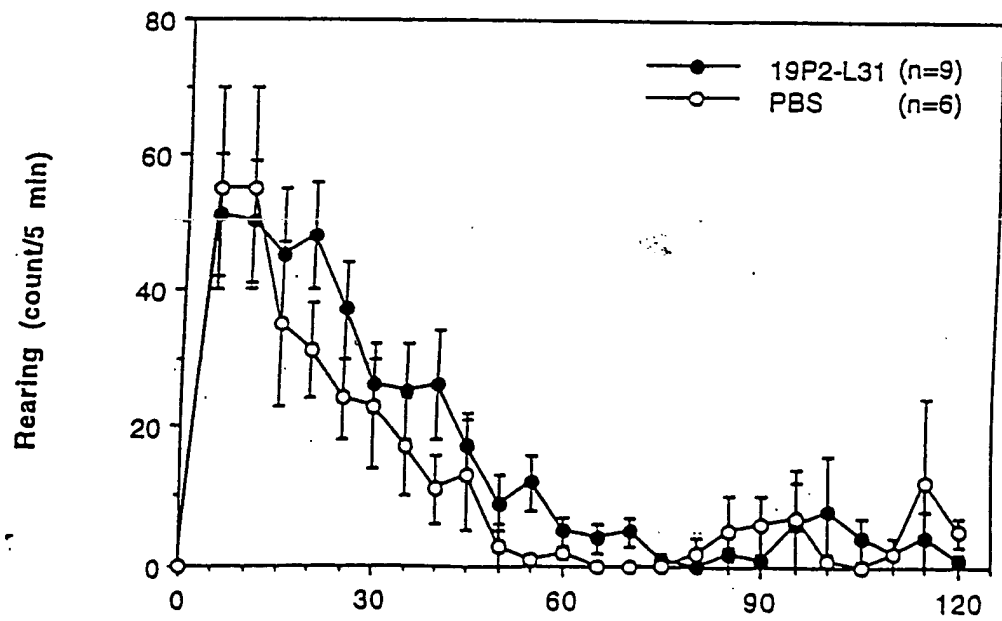
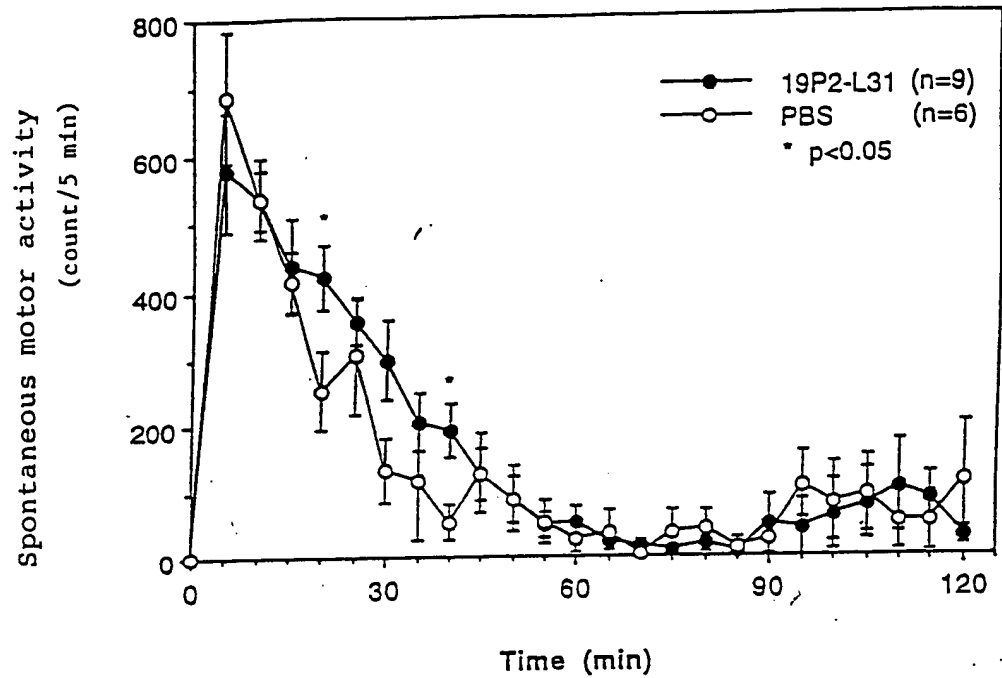


Fig. 44

(a)



(b)

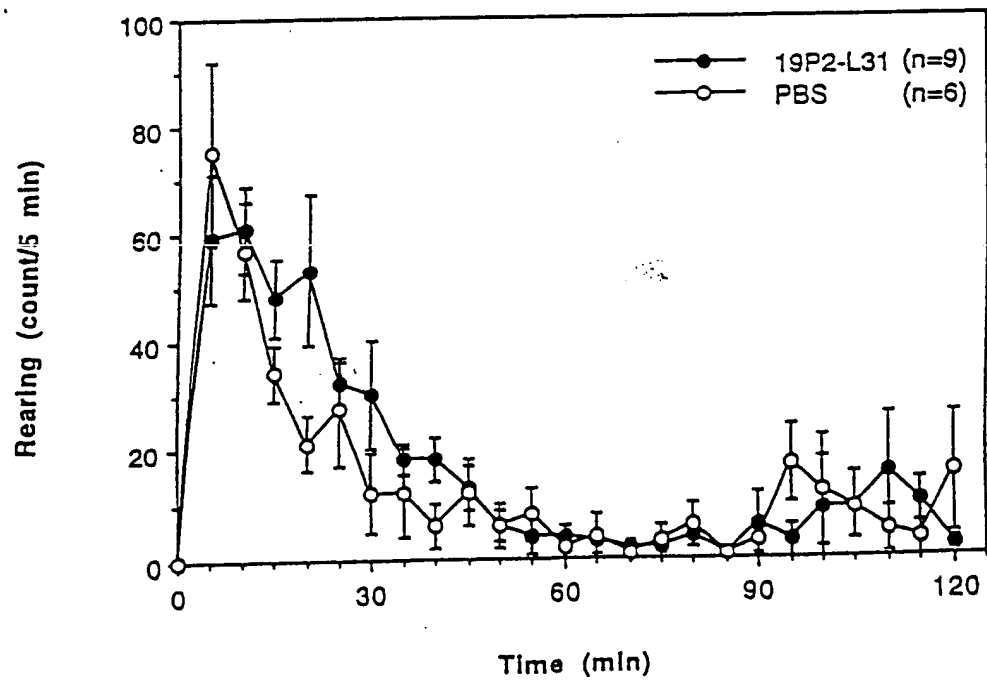


Fig. 45

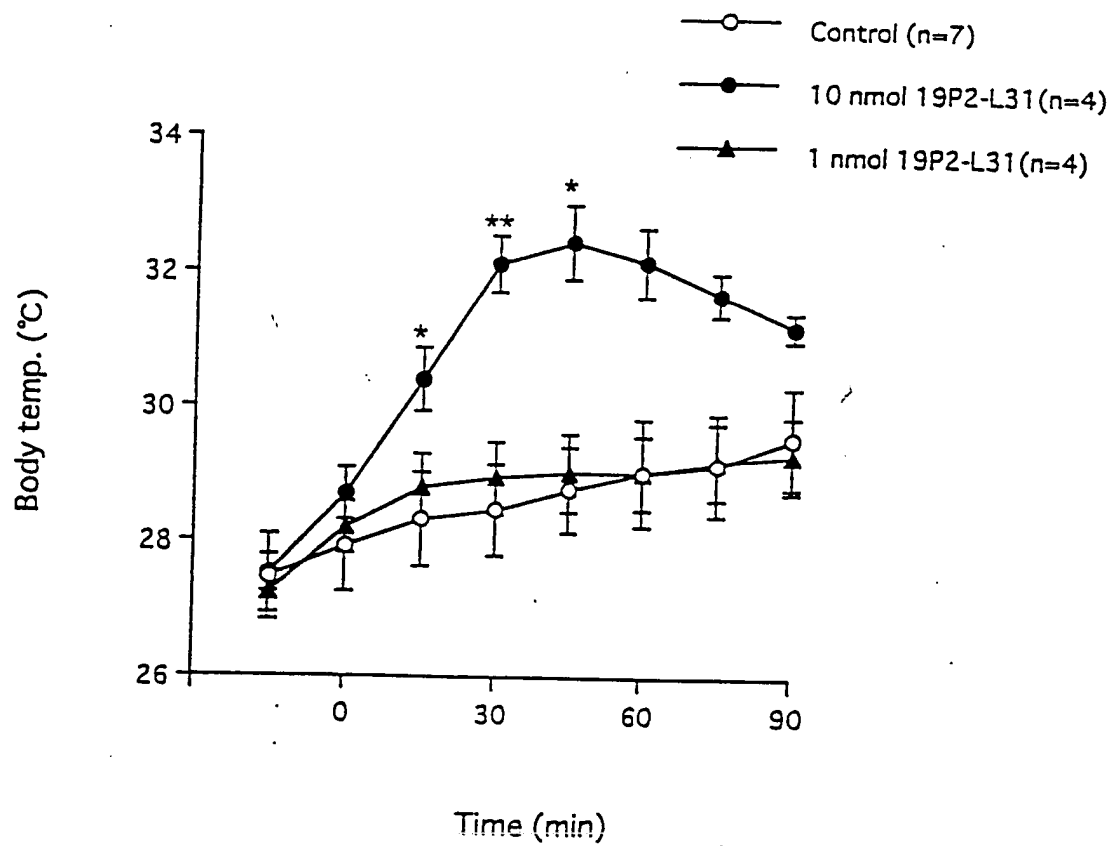
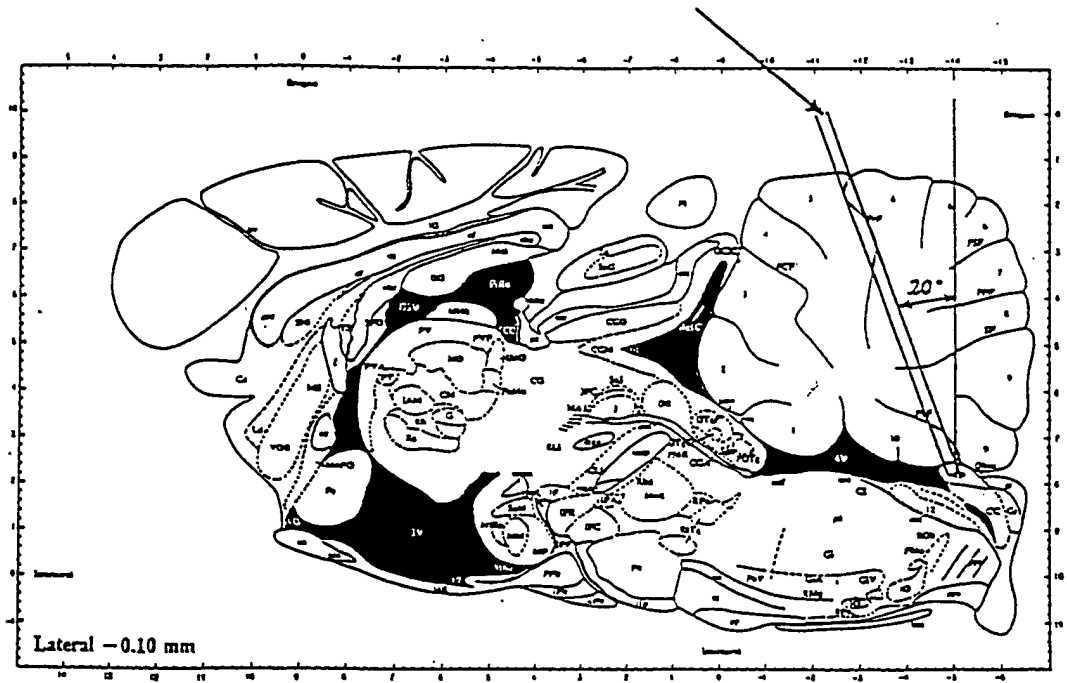
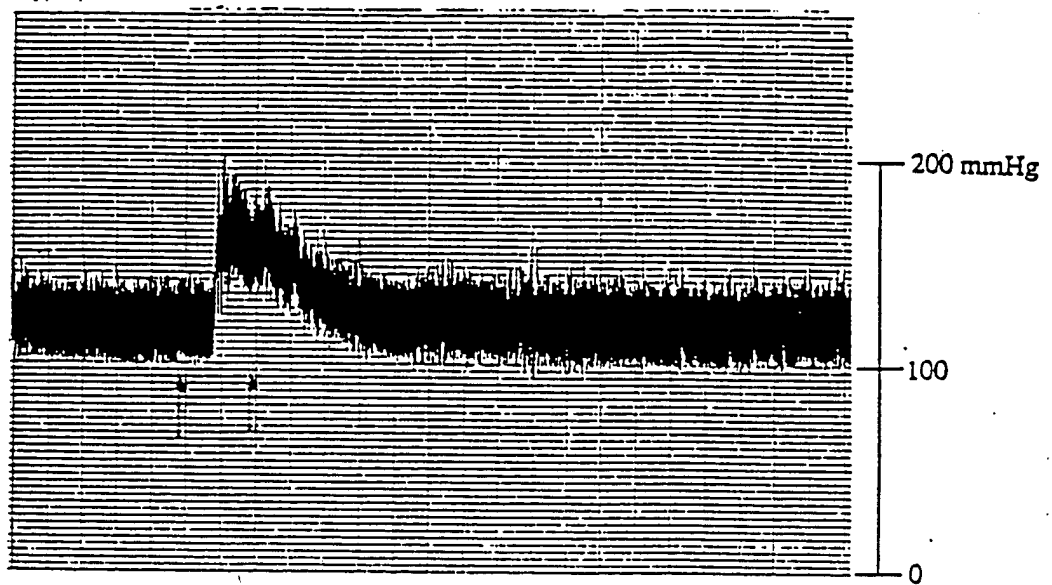


Fig. 46

micro-injection cannula



direct blood pressure



mean blood pressure

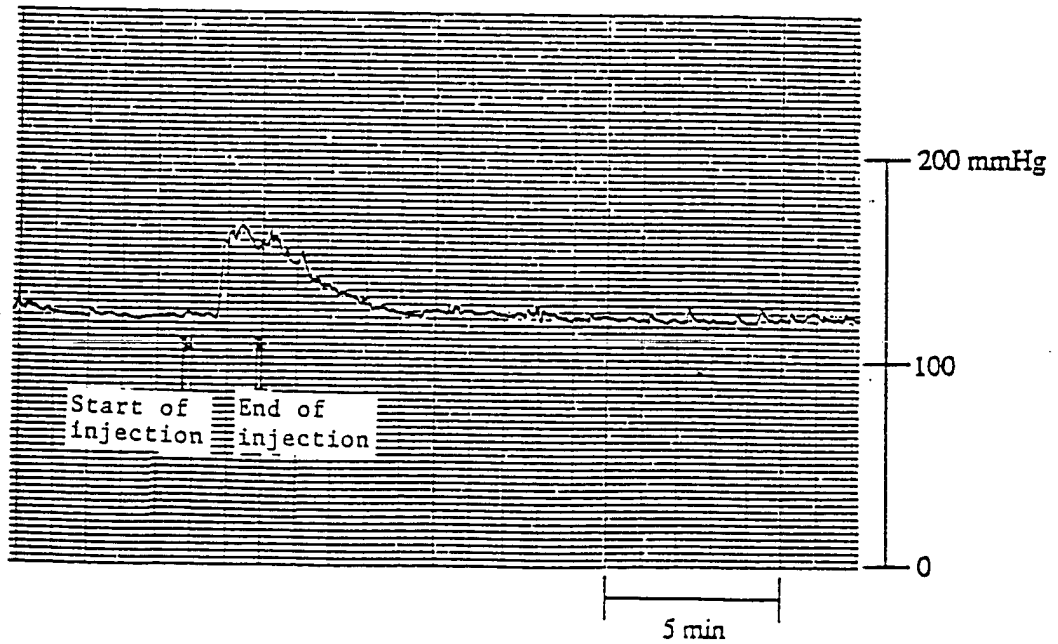


Fig. 48

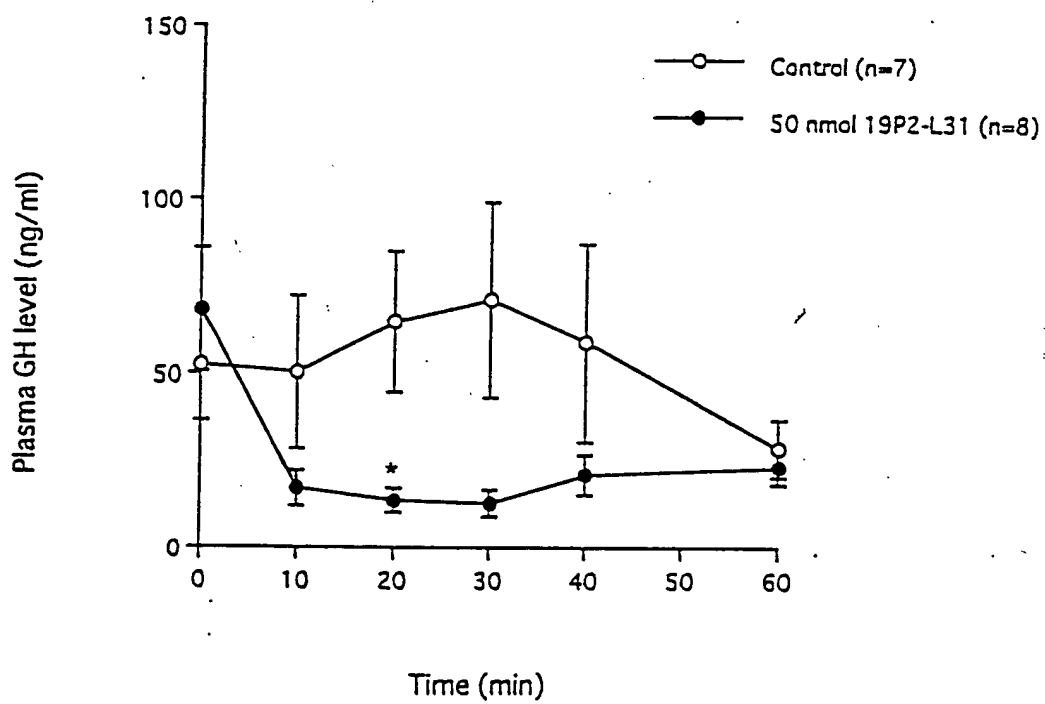


Fig. 49

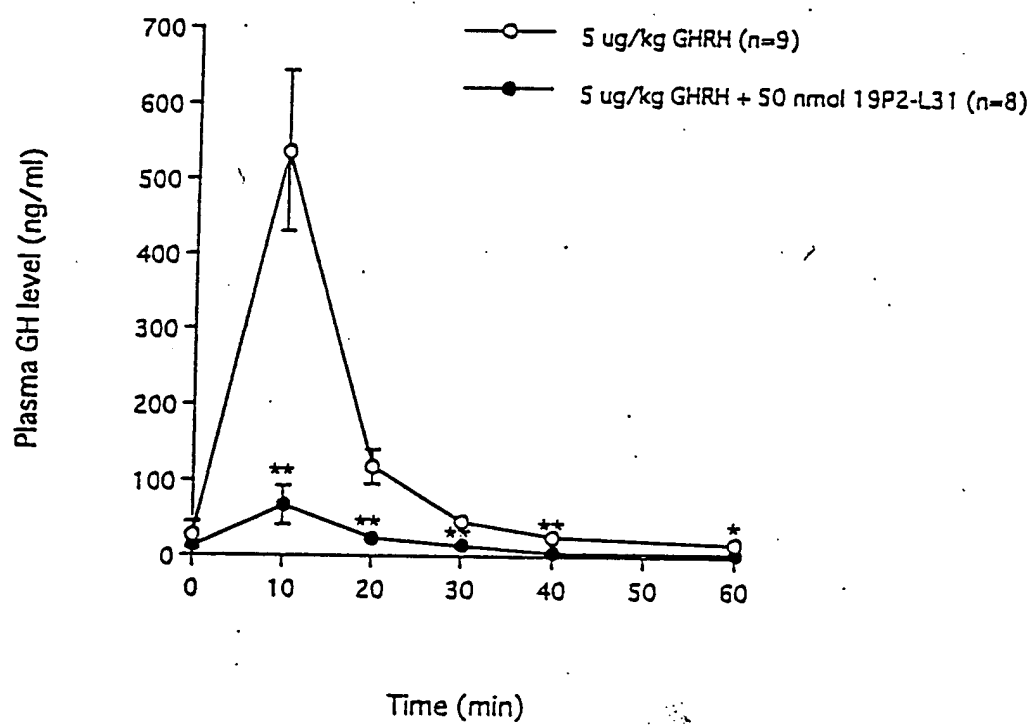


Fig. 50

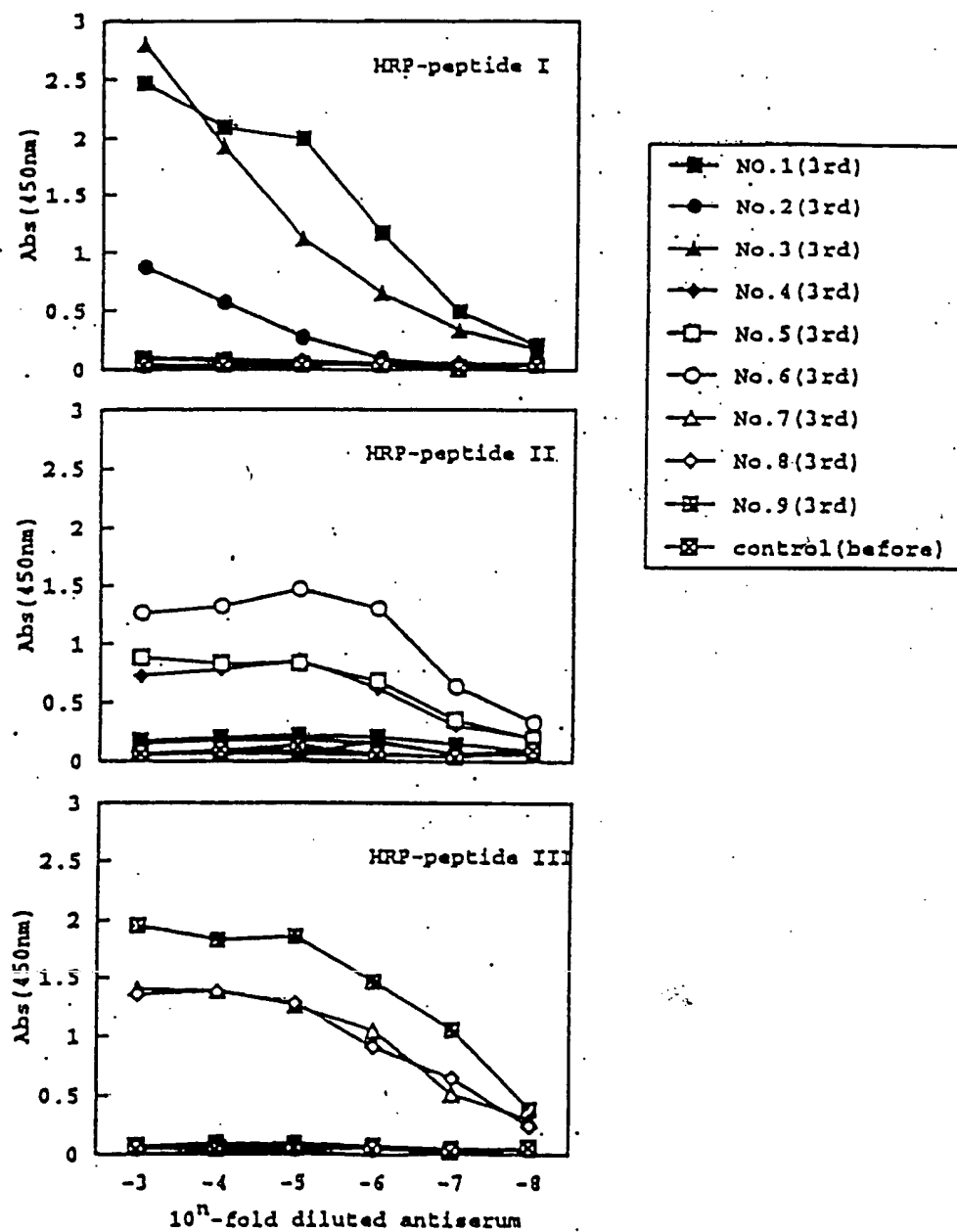
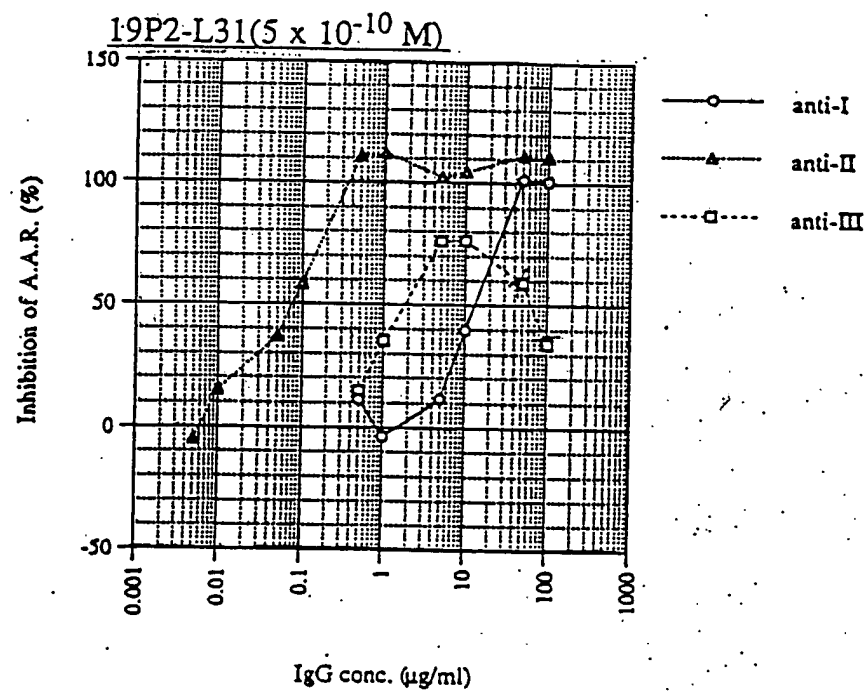


Fig. 51



000250" 06294560

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 5 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|